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[FR/FR]; 971, chemin du Tardinaou, F-13190 Allauch (FR).

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(74) Agents: **BRESE, Pierre et al.**; Brese-Majerowicz, 3, avenue de l'Opéra, F-75001 Paris (FR).

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(71) Applicant (for all designated States except US): **IPSO-GEN [FR/FR]**; 232 Boulevard Sainte-Marguerite, F-13273 Marseille Cedex 09 (FR).

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(72) Inventors; and

(75) Inventors/Applicants (for US only): **BERTUCCI, François [FR/FR]**; Le Sully, Parc de la Cadenelle, 122, rue du Commandant Rolland, F-13008 Marseille (FR). **HOULGATTE, Rémi [FR/FR]**; 31, Boulevard Lombard, F-13015 Marseille (FR). **BIRNBAUM, Daniel [FR/FR]**; 9, rue Baldacchini, La Croix-du-Sud, F-13009 Marseille (FR). **NGUYEN, Catherine [FR/FR]**; 8 Boulevard de la Kabylie, F-13016 Marseille (FR). **VIENS, Patrice [FR/FR]**; La Palmeraie Borely, Entrée A, 70, avenue d'Haïfa, F-13008 Marseille (FR). **FERT, Vincent**

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(54) Title: **GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE GENES**

(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1-468 or the complement thereof. The invention relates also to polynucleotide arrays useful to differentiate tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.

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GENE EXPRESSION PROFILING OF PRIMARY BREAST
CARCINOMAS USING ARRAYS OF CANDIDATE GENES

This invention relates to polynucleotide analysis
and, in particular, to polynucleotide expression profiling of
carcinomas using arrays of candidate polynucleotides.

Pathologists and clinicians in charge of the
management of breast cancer patients are facing two major
problems, namely the extensive heterogeneity of the disease
and the lack of factors - among conventional histological and
clinical features - predicting with reliability the evolution
of the disease and its sensitivity to cancer therapies.
Breast tumors of the same apparent prognostic type vary
widely in their responsiveness to therapy and consequent
survival of the patient. New prognostic and predictive
factors are needed to allow an individualization of therapy
for each patient.

Great hope is currently being placed on molecular
studies, which address the problem in a global fashion.
Methods such as cytogenetics, comparative genomic
hybridization, and whole-genome allelotyping have addressed
the issue at the genome level. Currently, the modifications
that take place in human tumors at the level of transcription
can also be studied in a large, unprecedented scale, using
new methods such as cDNA arrays that allow quantitative
measurement of the mRNA expression levels of many genes
simultaneously. Thus, it would be advantageous to provide a
means to assess the capacity of cDNA array testing in
clinical practice to better classify an heterogeneous cancer
into tumor subtypes with more homogeneous clinical outcomes,
and to identify new potential prognostic factors and
therapeutics targets.

The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences or subsequences thereof wherein the sequences or subsequences are either underexpressed or overexpressed in tumor cells, further wherein the sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 468 or the complement thereof.

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples.

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma.

Fig. 3 is prognostic classification of breast cancer by gene expression profiling.

Fig. 4 shows the correlation of GATA3 expression with ER phenotype.

In the context of this disclosure, a number of terms shall be utilized.

The term "polynucleotide" refers to a polymer of RNA or DNA that is single-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer sequence of nucleic acids.

The term "immobilized on a support" means bound directly or indirectly thereto including attachment by

covalent binding, hydrogen bonding, ionic interaction, hydrophobic interaction or otherwise.

Breast cancer is characterized by an important histoclinical heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. An important object of the present invention relates to a large-scale molecular characterization of breast cancer that could help in prediction, prognosis and cancer treatment.

An important aspect of the invention relates to the use of cDNA arrays, which allows to quantitative study mRNA expression levels of 188 candidate genes in 34 consecutive primary breast carcinomas along three directions: comparison of tumor samples, correlations of molecular data with conventional histoclinical prognostic features and gene correlations. The experimentation evidenced extensive heterogeneity of breast tumors at the transcriptional level. Hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clinical outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclinical parameters. No correlation was found with the age of patients, tumor size, histological type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ($p \leq 0.0001$) and that of GATA3 with the presence of estrogen receptors ($p \leq 0.001$). Thus, experimental results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA

array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

5 DNA arrays consist of large numbers of DNA molecules spotted in a systematic order on a solid support or substrate such as a nylon membrane, glass slide, glass beads or a silicon chip. Depending on the size of each DNA spot on the array, DNA arrays can be categorized as microarrays (each
10 DNA spot has a diameter less than 250 microns) and macroarrays (spot diameter is greater than 300 microns). When the solid substrate used is small in size, arrays are also referred to as DNA chips. Depending on the spotting technique used, the number of spots on a glass microarray can
15 range from hundreds to thousands.

DNA microarrays have serve a variety of purposes, including, gene expression profiling, de novo gene sequencing, gene mutation analysis, gene mapping and genotyping. cDNA microarrays are printed with distinct cDNA
20 clones isolated from cDNA libraries. Therefore, each spot represents an expressed gene, since it is derived from a distinct mRNA.

Typically, a method of monitoring gene expression involves providing (1) providing a pool of sample
25 polynucleotides comprising RNA transcript(s) of one or more target gene(s) or nucleic acids derived from the RNA transcript(s); (2) reacting, such as hybridizing the sample polynucleotide to an array of probes (for example, polynucleotides obtained from a polynucleotide library)
30 (including control probes) and (3) detecting the reacted/hybridized polynucleotides. Detection can also involve calculating/quantifying a relative expression (transcription) level.

The present invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 in annex or the complement thereof.

Obviously, sequences having a great degree of homology with the above sequences could also been used to realize the molecular characterization of the invention, namely when those sequences present one or a few punctual mutations when compared with anyone of sequences SEQ ID Nos: 1 - 468.

The invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 249 (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) or the complement thereof

Preferably the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 247 (Here, these SEQ ID N° refer to old SEQ ID N° 1-247 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application

in annex); further wherein said sequences are useful in differentiating a normal cell from a cancer cell.

5 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 242 (Here, these SEQ ID N° refer to old SEQ ID N° 1-242 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex);
10 wherein said sequences are useful in detecting a hormone sensitive tumor cell, or wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

15 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 224; (Here, these SEQ ID N° refer to old SEQ ID N° 1-224 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) wherein said sequences are useful in differentiating tetracycline-sensitive tumors from tetracycline-insensitive tumors.
20

25 The invention relates also to any polynucleotide library as previously described wherein said polynucleotides are immobilized on a solid support in order to form a polynucleotide array.

30 Preferably the support is selected from the group consisting of a nylon membrane, glass slide, glass beads, or a silicon chip.

The invention concerns also a method for detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

- a) obtaining a polynucleotide sample from a patient; and
- 5 b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously described or an expression product encoded by any of the polynucleotide sequences of said
- 10 libraries and
- c) detecting the reaction product of step (b).

The invention relates also to a such method for detecting differentially expressed polynucleotide sequences

15 of the invention wherein the amount of reaction product of step (c) is compared to a control sample.

Preferably the polynucleotide sample isolated for, the sample is RNA or mRNA.

Preferably the polynucleotide sample is cDNA obtained by

20 reverse transcription of the mRNA.

In a preferred embodiment the method for detecting differentially expressed polynucleotide sequences, the step (b) comprises a hybridization of the sample RNA with the labeled probe.

25 The method for detecting differentially expressed polynucleotide sequences is used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and namely breast cancer.

30 The method for detecting differentially expressed polynucleotide sequences is particular useful wherein the product encoded by any of the polynucleotide sequences or

subsequences is involved in a receptor-ligand reaction on which detection is based.

5 The invention relates also to a method for screening an anti-tumor agent comprising the method for detecting differentially expressed polynucleotide sequences previously described wherein the sample has been treated with the anti-tumor agent to be screened.

10 Le label used to label polynucleotide samples is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent label.

15 The invention also relates to a library of polynucleotides comprising a population of polynucleotide sequences overexpressed or underexpresses in cells derived from a tumor selected from SEQ ID NO :1 to SEQ ID NO :249 and their respective complements. (Here, these SEQ ID N° refer
20 to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex).

25 In a particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ;
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 28 ; SEQ ID No : 29 ;
SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 45 ;
SEQ ID No : 46 ; SEQ ID No : 52 ; SEQ ID No : 54 ; SEQ ID No :
63 ; SEQ ID No : 64 ; SEQ ID No : 81 ; SEQ ID No : 82 ; SEQ ID No :
87 ; SEQ ID No : 88 ; SEQ ID No : 101 ; SEQ ID No : 102 ; SEQ ID
30 No : 103 ; SEQ ID No : 104 ; SEQ ID No : 105 ; SEQ ID No : 107 ;
SEQ ID No : 113 ; SEQ ID No : 114 ; SEQ ID No : 115 ; SEQ ID No :
116 ; SEQ ID No : 127 ; SEQ ID No : 128 ; SEQ ID No : 131 ; SEQ
ID No : 139 ; SEQ ID No : 140 ; SEQ ID No : 142 ; SEQ ID No : 150 ;
SEQ ID No : 151 ; SEQ ID No : 154 ; SEQ ID No : 156 ; SEQ ID

No : 160 ; SEQ ID No : 161 ; SEQ ID No : 162 ; SEQ ID No : 177 ;
SEQ ID No : 178 ; SEQ ID No : 194 ; SEQ ID No : 195 ; SEQ ID No :
227 ; SEQ ID No : 228 ; SEQ ID No : 229 ; SEQ ID No : 231 ; SEQ ID
No : 233 ; SEQ ID No : 243 ; SEQ ID No : 244 ; SEQ ID No : 245 ;
5 SEQ ID No : 246 ; SEQ ID No : 247, (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 5 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex),
which distinguish a healthy person from a person with cancer.

10 Preferably the invention relates to
polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID
No : 102 ; SEQ ID No : 103 ; SEQ ID No : 107 ; SEQ ID No : 229 ;
SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 243 ; SEQ ID No :
244 ; SEQ ID No : 245 ; SEQ ID No : 246 ; SEQ ID No : 247 (Here,
15 these SEQ ID N° refer to old SEQ ID N° presented on table 6
in priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex), which distinguish a healthy
person from a person with cancer.

20 In another particular embodiment the invention relates
to polynucleotide sequences: SEQ ID No : 2 ; SEQ ID No : 3 ;
SEQ ID No : 4 ; SEQ ID No : 5 ; SEQ ID No : 6 ; SEQ ID No : 7 ;
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 10 ; SEQ ID No : 11 ;
25 SEQ ID No : 12 ; SEQ ID No : 13 ; SEQ ID No : 14 ; SEQ ID No : 15
; SEQ ID No : 16 ; SEQ ID No : 17 ; SEQ ID No : 18 ; SEQ ID No :
19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No
: 23 ; ; SEQ ID No : 24 ; SEQ ID No : 25 ; SEQ ID No : 26 ; SEQ ID
No : 27 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 223 ;
30 SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer
to old SEQ ID N° presented on table 7 in priority document,
the correlation table 10 allows to identify these sequences
in the sequence listing of the present application in annex)
which detect hormone sensitive tumors.

Preferably the invention relates to polynucleotide sequences SEQ ID No : 1; SEQ ID No : 2 SEQ ID No : 3; SEQ ID No : 4; SEQ ID No : 5; SEQ ID No : 221; SEQ ID No : 222 ; SEQ ID No : 15; SEQ ID No : 16; SEQ ID No : 17; SEQ ID No : 18 ; SEQ ID No : 19; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 241; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which detect hormone sensitive tumors.

In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 3 ; SEQ ID No : 4 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 23 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 33 ; SEQ ID No : 34 ; SEQ ID No : 35 ; SEQ ID No : 36; SEQ ID No : 37; SEQ ID No : 38; SEQ ID No : 39; SEQ ID No : 40 ; SEQ ID No : 41 ; SEQ ID No : 42 ; SEQ ID No : 43 ; SEQ ID No : 44 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 233 ; SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

Preferably the invention relates to polynucleotide sequences : SEQ ID No : 1 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No : 28; ; SEQ ID No : 29 ; SEQ ID No : 29 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 37 ; SEQ ID No : 38 ; SEQ ID No : 39 ; SEQ ID No : 241 ; SEQ ID No : 241, (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to

identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

5 In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 2 ;
SEQ ID No : 6 ; SEQ ID No : 7 ; SEQ ID No : 8 ; SEQ ID No : 9 ;
SEQ ID No : 10 ; SEQ ID No : 11 ; SEQ ID No : 13 ; SEQ ID No : 14
10 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No :
22 ; SEQ ID No : 23 ; SEQ ID No : 35 ; SEQ ID No : 36 ; ; SEQ ID
No : 37 ; SEQ ID No : 56 ; SEQ ID No : 57 ; SEQ ID No : 74 ; SEQ
ID No : 75 ; SEQ ID No : 102 ; SEQ ID No : 104 ; SEQ ID No : 107
; SEQ ID No : 108 ; SEQ ID No : 109 ; SEQ ID No : 118 ; SEQ ID No
: 119 ; ; SEQ ID No : 136 ; SEQ ID No : 213 ; SEQ ID No : 214 ;
15 SEQ ID No : 215 ; SEQ ID No : 223 ; SEQ ID No : 224 (Here, these
SEQ ID N° refer to old SEQ ID N° presented on table 11 in
priority document, the correlation table 10 allows to
identify these sequences in the sequence listing of the
present application in annex) which distinguish tumors
20 sensitive to anthracycline from tumors unsensitive to
anthracycline.

 The invention relates also to a method of detecting
differentially expressed genes correlated with a cancer
25 comprising detecting at least one library of polynucleotide
sequences as above defined or of products encoded by said
library in a sample obtained from a patient.

 A particular embodiment of the invention relates
30 to a polynucleotide library of corresponding substantially to
any combination of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets 1 to set 212 as defined in
table 4

The invention relates obviously to polynucleotide libraries comprising at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of said predefined sets, allowing to obtain a discriminating gene pattern, namely to distinguish between normal patients and patients suffering from tumor pathology, between patients having an hormone sensitive tumor and patients having an hormone resistant tumor, between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes, between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor and between patients having good prognosis primary breast tumors and patients having poor prognosis primary breast tumors.

Polynucleotide sequences library useful for the realization of the invention can comprise also any sequence comprised between 3'end and 5'end of each polynucleotide sequence set as defined in table 4, allowing the complete detection of the implicated genes.

The invention relates also to a polynucleotide library useful to differentiate a normal cell from a cancer cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

Preferably the polynucleotide library useful to differentiate a normal cell from a cancer cell correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated in table 5B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 5A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 5B allows to distinguish between normal patients, and patients suffering from tumor pathology.

The invention relates also to a polynucleotide library useful to detect a hormone sensitive tumor cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

Preferably the polynucleotide library useful to detect a hormone sensitive tumor cell correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 6A, together with detection of an underexpression of

genes identified with sets of polynucleotides sequences defined in table 6B allows to distinguish between patients having an hormone sensitive tumor and patients having an hormone resistant tumor.

5

The invention concerns also a polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 7A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 7B allows to distinguish between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes.

The invention concerns also a polynucleotide library useful to differentiate anthracycline-sensitive tumors

from anthracycline-insensitive tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide library useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 8A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 8B allows to distinguish between patients having an anthracycline-sensitive tumor from patients having an anthracycline-insensitive tumor.

The invention concerns also a polynucleotide library useful to classify good and poor prognosis primary breast tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide library useful to classify good and poor prognosis primary breast tumors correspond substantially to any combination of at least one

polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 9A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 9B allows to classify patients having good and poor prognosis primary breast tumors.

In a preferred embodiment, the tumor cell presenting underexpressed or overpressed sequences from the polynucleotide library of the invention are breast tumor cells.

In a particular embodiment the polynucleotides of the polynucleotide library of the present invention are immobilized on a solid support in order to form a polynucleotide array, and said solid support is selected from the group consisting of a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

Another object of the present invention concerns a polynucleotide array useful for prognosis or diagnostic of tumor comprising at least one immobilized polynucleotide library set as previously defined.

Then the invention concerns a polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of at least one polynucleotide sequence selected among those included in each

one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

5 Preferably the polynucleotide array useful to differentiate a normal cell from a cancer cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each
10 one of predefined polynucleotide sequences sets indicated in table 5B.

The invention relates also to a polynucleotide array useful to detect a hormone sensitive tumor cell
15 comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

20 Preferably the polynucleotide array useful to detect a hormone sensitive tumor cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in
25 table 6B.

The invention concerns also a polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of at
30 least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The invention concerns also a polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The invention concerns also a polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide array useful to classify good and poor prognosis primary breast tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The present invention concerns also a method for detecting differentially expressed polynucleotide sequences that are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously defined or an expression product encoded by any of the polynucleotide sequences of the libraries previously defined

c) detecting the reaction product of step (b).

Preferably, the polynucleotide sample obtained at step (a) is labeled before its reaction at step (b) with the probe immobilized on a solid support.

The label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

In a particular embodiment the reaction product of step (c) is quantified by further comparison of said reaction product to a control sample.

5 In a first embodiment, the polynucleotide sample isolated from the patient and obtained at step (a) is either RNA or mRNA.

In another embodiment the polynucleotide sample isolated from the patient is cDNA is obtained by reverse transcription of the mRNA.

10 Preferably the reaction step (b) of the method for detecting differentially expressed polynucleotide sequences comprises a hybridization of the sample RNA issued from patient with the probe.

15 Preferably the sample RNA is labeled before hybridization with the probe and the label is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

20 This method for detecting differentially expressed polynucleotide sequences is particularly useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and particularly breast cancer.

25 The method for detecting differentially expressed polynucleotide sequences is also particularly useful when the product encoded by any of the polynucleotide sequences or subsequences set is involved in a receptor-ligand reaction on which detection is based.

30 The present invention is also related with a method for screening an anti-tumor agent comprising the method the above-depicted method for detecting differentially expressed polynucleotide sequences wherein the sample has been treated with the anti-tumor agent to be screened.

In a particular embodiment the method for screening an anti-tumor agent comprises detecting polynucleotide sequences reacting with at least one library of polynucleotides or polynucleotide sequences set as previously defined or of products encoded by said library in a sample obtained from a patient.

The invention is illustrated by examples detailed below related to particular experimental results obtained with selected libraries of polypeptides useful to identify and distinguish tumor samples from normal ones.

Tumor samples and RNA extraction

To avoid any bias of selection as to the type and size of the tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 34 patients undergoing surgery at the Institute Paoli-Calmette. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis and an adjacent piece was quickly frozen in liquid nitrogen for molecular analyses. The median age of patients at the time of diagnosis was 55 years (range 39, 83) and most of them were post-menopausal. Tumors were classified according to the WHO histological typing of breast tumors in: 29 ductal carcinomas, 2 lobular carcinomas, 1 mixed ductal and lobular carcinoma, and 2 medullar carcinomas. They had various sizes, inferior or equal to 20 mm (n = 13), between 20 and 50 mm (n = 18) or superior to 50 mm (n = 3), axillary's lymph node status (negative: 19 tumors, positive: 15 tumors), SBR grading (I: 3 tumors, II: 20 tumors, III: 10 tumors, not evaluable: 1 tumor), and estrogen receptor status (ER) evaluated by

immunohistochemical assay (23 ER-positive, 11 ER-negative). ER positivity cutoff value was 10%. Adjuvant treatment with radiotherapy and when necessary multi-agent anthracyclin-based chemotherapy (n = 16) was given to patients according to local practice.

Total RNA was extracted from tumor samples by standard methods (43). Total RNA from normal breast tissue was obtained from Clontech (Palo Alto, CA): RNA was isolated from 8 tissue specimens from Caucasian females, age range 23 - 47. RNA integrity was controlled by denaturing formaldehyde agarose gel electrophoresis and Northern blots using a 28S-specific oligonucleotide.

cDNA arrays preparation

Gene expression was analyzed by hybridization of arrays with radioactive probes. The arrays contained PCR products of 5 control clones, and 180 IMAGE human cDNA clones selected with practical criteria (3' sequence of mRNA, same cloning vector, host bacteria and insert size). This represented 176 genes (4 genes were represented by 2 different clones): 121 with proven or putative implication in cancer and 55 implicated in immune reactions (the list is available on the web site: <http://tagc.univ-mrs.fr/pub/Cancer/>). Their identity was verified by 5' tag-sequencing of plasmid DNA and comparison with sequences in the EST (dbEST) and nucleotide (GenBank) databases at the NCBI. Identity was confirmed for all but 14 clones without significant gene similarity, which were referenced by their GenBank accession number. The control clones were: Arabidopsis thaliana cytochrome c554 gene (used for hybridization signal normalization), 3 poly(A) sequences of different sizes and the vector pT7T3D (negative controls).

PCR amplification, purification and robotical spotting of PCR products onto Hybond-N+ membranes (Amersham) were done according to described protocols (4). All PCR products were spotted in duplicate. For normalization purpose, the c554 gene was spotted 96-fold scattered over the whole membrane.

cDNA array hybridizations

Hybridizations were done successively with a vector oligonucleotide (to precisely determine the amount of target DNA accessible to hybridization in each spot), then after stripping of vector probe, with complex probes made from the RNAs (4). Each complex probe was hybridized to a distinct filter. Probes were prepared from total RNA with an excess of oligo(dT25) to saturate the poly(A) tails of the messengers, and to insure that the reverse transcribed product did not contain long poly(T) sequences. A precise amount of c554 mRNA was added to the total RNA before labeling to allow normalization of the data.

Five ng of total RNA (~100ng of mRNA) from tissue samples were used for each labeling. Probe preparation and hybridization of the membranes were done according to known procedures (<http://tagc.univ-mrs.fr/pub/Cancer/>).

Hybridization was done in excess of target (~15 ng of DNA in each spot) and binding of cDNAs to the targets was linear and proportional to the quantity of cDNA in the probe.

Detection and quantification of cDNA array hybridization signals

Quantitative data were obtained using an imaging plate device. Hybridization signal detection with a FUJI BAS 1500 machine and quantification with the HDG Analyzer

software (Genomic Solutions, Ann Arbor, MI) were done as previously described (<http://tagc.univ-mrs.fr/pub/Cancer/>). Quantification was done by integrating all spot pixel intensities and subtracting a spot background value determined in the neighboring area. Spots were located with a Laplacian transformation. Spot background level was the median intensity of all the pixels present in a small window centered on the spot and which were not part of any spot (44). Quantified data were normalized in three steps and expressed as absolute gene expression levels (i.e. in percentage of abundance of individual mRNA with respect to mRNA within the sample), as described (4).

Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridization with the same probe on two independent arrays, or two independent hybridizations with probes prepared from the same RNA. In every case, the results showed good reproducibility with respective correlation coefficients of 0.95, 0.98 and 0.98 (data not shown). Moreover, genes represented by two different clones on the array, such as CDK4 or ETV5, displayed similar expression profiles for the two clones in all samples. This reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential.

For graphical representation, data were displayed as absolute expression levels (Fig. 2a). For better visualization of clustering, results were log-transformed and displayed as relative values median-centered in each row and in each column (Fig. 2b). Hierarchical clustering was applied to the tissue samples and the genes using the Cluster program developed by Eisen (45) (average linkage clustering

using Pearson correlation as similarity metric). Results in Figs. 2 and 3 were displayed with the TreeView program (45).

Subsequent analysis was done using Excel software (Microsoft) and statistical analyses with the SPSS software. Metastasis-free survival and overall survival were measured from diagnosis until the first metastatic relapse or death respectively. They were estimated with the Kaplan-Meier method and compared between groups with the Log-Rank test. Correlations of gene pairs based on expression profiles were measured with the correlation coefficient r . The search for genes with expression levels correlated with tumor parameters was done in several successive steps.

First, genes were detected by comparing their median expression level in the two subgroups of tumors discordant according to the parameter of interest. The median values rather than the mean values were used because of the high variability of the expression levels for many genes, resulting in a standard deviation of expression level similar or superior to the mean value and making comparisons with means impossible. Second, these detected genes were inspected visually on graphics, and finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of GATA3 expression between ER-positive tumors and ER-negative tumors was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels to the number of axillary nodes involved.

Northern blot analysis

Seventy-nine breast tumors, including 22 of the 34 tested on the arrays, were analyzed for GATA3 expression by Northern blot hybridization. RNA extraction from tumor samples and Northern blots were done as previously described

(43). The GATA3 probe was prepared from the IMAGE cDNA clone 129757, which corresponds to the 3' region (from +843 to +1689) of the GATA3 cDNA sequence (GenBank accession no. X55122). The insert (846 bp) was obtained by digestion of the clone with EcoRI and PacI enzymes. Northern blots were stripped and re-hybridized using a α -actin probe (46).

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples. Each cDNA array on Nylon filter was hybridized with a complex probe made from 5 μ g of total RNA. The top image corresponds to the whole membrane. For the two bottom images, only the right portion of the membranes is shown. Numbers below the spots indicate housekeeping genes (1, GAPDH and 2, actin), negative control clones (3, 4 and 5) and examples of genes differentially expressed between NB and breast tumor (6, stromelysin3; 7, ERBB2; 8, MYBL2; 9, FOS; 10, TGF β 3; 11, desmin), and between ER- breast tumor and ER+ breast tumor (12, GATA3).

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma. Each column corresponds to a single tissue, and each row to a single gene. (a) The results are expressed as percentage abundance of individual mRNA within the sample, and are represented using a blue color scale. The color scale (log scale with a 3-fold interval) indicated at the bottom left ranges from light blue (expression level 0.001%) to dark blue (expression level > 3%). White squares indicate clones with undetectable expression levels and gray squares indicate missing data. The tissue samples are arbitrarily ordered and the clones are ordered from top to bottom according to increasing median expression levels. Horizontal black arrows on the right of the figure mark three clones with highly variable expression levels between the

tumors (stromelysin3, IGF2, GATA3 from top to bottom). (b) The results are shown as relative expression levels (relative to the median value of each row and each column) and are represented with a color scale indicated at the bottom left ranging from 1/100 to 100 fold changes (gray squares: missing data). Eighteen clones with median expression level equal to zero in the 34 tumors are omitted. The clustering program arranges samples ($n = 35$) along the horizontal axis so that those with the most similar expression profiles are placed adjacent to each other. Similarly, clones ($n = 162$) are near each other along the vertical axis if they show a strong expression profile correlation across all tissues. The length of the branches of the dendrograms capturing respectively the samples (top) and the clones (left) reflects the similarity of the related elements. Two groups of tumors are separated and color coded: group A (blue) and group B (orange). Horizontal black and horizontal red arrows on the right of the figure respectively mark three genes with highly variable expression levels between the tumors (IGF2, GATA3, stromelysin3 from top to bottom) and four pairs of different clones representing four genes. (c) Zoom representation of group A from Figure 2b, excluding the two outlier tumors at the right. The clustering separates two subgroups of tumors, A1 and A2. The dotted branches correspond to tumors associated with metastatic relapse and death. Follow-up was longer in A2 than in A1 (median 81 months vs 47 for A1).

Fig. 3 is prognostic classification of breast cancer by gene expression profiling showing that gene expression-based tumour classification correlates with clinical outcome. The 12 samples of group A (see figure 2b and 2c) were reclustered using the top 32 differentially expressed genes between A1 and A2 subgroups. Data were displayed as in Fig. 2b and shown with the same color key.

The hierarchical clustering was applied to expression data from the 23 clones, out of 32, of which expression levels presented an at least two-fold change in at least two samples (out of 12). Two subgroups of tumors A1 and A2 are shown as well as two groups of differentially expressed clones. The dotted branches of tumor cluster A1 correspond to samples associated with metastatic relapse and death. Figure 3a shows Two-dimensional representation of hierarchical clustering results shown in figures 2a and 2b. The analysis delineates 4 groups of tumours A, B, C and D. Black squares indicate patients alive at last follow-up visit and red squares indicate patients who died. Three classes of patients with a statistically different clinical outcome were defined according to gene expression profiles: class A (n = 16), class B+C (n = 34), class D (n = 5). Figure 3b illustrates Kaplan-Meier plot of overall survival of the 3 classes of patients ($p < 0.005$, log-rank test). And figure 3c illustrates Kaplan-Meier plot of metastasis-free survival of the 3 classes of patients ($p < 0.05$, log-rank test).

Fig. 4 shows the correlation of GATA3 expression with ER phenotype. (a) The expression levels of GATA3 in 34 breast cancer samples (y axis) monitored by cDNA array analysis are reported in percentage of abundance of individual mRNA with respect to mRNA within the sample (log scale). GATA3 is significantly overexpressed in the ER-positive tumors (n = 23) versus the ER-negative tumors (n = 11) using the Mann-Witney test ($p = 0.0004$). The expression level of GATA3 in normal breast tissue is reported on the right (NB). (b) Northern blot analysis of GATA3 in normal breast sample (NB) and 9 breast cancer samples (AT: tumor analyzed with cDNA array and Northern blot; NT: tumor analyzed with Northern blot). Blots were probed successively

with cDNA from GATA3 (top) and α -actin (bottom). ER status is indicated for each tumor sample.

Data representation

5 Fig. 1 shows examples of hybridizations of cDNA arrays with probes made from RNA extracted from normal breast tissue and breast tumors.

10 The crude results of all hybridizations were processed to be presented either as absolute or relative values in schematic figures. The normalization procedure allowed display of absolute values expressed in percent of abundance of mRNA in the probe as shown in Fig. 2a. Each level of the blue color ladder represents a 3-fold interval of absolute abundance of mRNA. Each column corresponds to a tissue sample and each row to a gene. For graphic purposes, genes were ordered from top to bottom according to increasing median expression levels. Tumor samples were not ordered. The values in each sample displayed a wide range of intensities (3 decades in log scale) corresponding to expression levels ranging from approximately 0.002% to 5% of mRNA abundance. Many genes (see for example stromelysin 3, IGF2 and GATA3, arrows) displayed highly variable expression levels across all tumor samples, scattered over the whole dynamic range of values. A representation of relative values is shown in Fig. 2b. Absolute values were log-transformed, omitting 18 clones whose median intensity was equal to zero across all tissues. Data for each of the 162 remaining clones were then median-centered, as well as data for each sample, so that the relative variation was shown, rather than the absolute intensity. A color scale was used to display data: red for expression level higher than the median and green for expression level lower than the median. The magnitude of the deviation from the median was represented by

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the color intensity. A hierarchical clustering program was then applied to group the 35 samples according to their overall gene expression profiles, and to group the 162 clones on the basis of similarity of their expression levels in all tissues. This resulted in a picture highlighting groups of correlated tissues and groups of correlated genes as depicted by dendrograms.

Breast tumor classification

As shown in Fig. 2b, the clustering algorithm identified two groups of samples, designated A ($n = 15$, including normal breast, NB) and B ($n = 20$). These groups were similar with respect to patient age, menopausal status at diagnosis, SBR grading and tumor pathological size. However, 72% of tumors in group A were node-positive and 75% in group B were node-negative. Moreover, 80% of the tumors in group B were estrogen receptor (ER) positive and 50% in group A were ER-negative. With a median follow-up of 44 months after diagnosis, overall survival was different between A and B groups: 5 women died in A (median follow-up 58 months) and 1 in B (median follow-up 40 months). But the frequency of metastatic relapse was relatively similar in the two groups, with 5 women who relapsed in A and 6 in B. Because the time between the diagnosis of metastasis and last follow-up is too short in B, a longer follow-up is needed to determine if these two different groups, defined with expression profiles, have really a different outcome with respect to overall survival.

In the group A of 15 samples, three samples (normal breast and two tumors) were different from each other and from the other 12 samples. The latter constituted two subgroups of tumors, A1 ($n = 6$) and A2 ($n = 6$), which could be further separated by clustering as shown in Fig. 2c. The

12 tumors had an uniformly high risk of metastatic relapse according to conventional prognostic features as shown in Table 1. Most of them had received comparable adjuvant anthracyclin-based chemotherapy after surgery, with more women treated in the A1 subgroup. Interestingly, these two subgroups, which could not be distinguished with commonly used histoclinical features, had a very different clinical outcome: there were 4 metastatic relapses and 4 deaths in A1 (median follow-up: 44 months). In contrast and despite a longer median follow-up (90 months), no metastasis or death occurred in A2. This resulted in a significant better metastasis-free survival ($p = 0.01$) and overall survival ($p = 0.005$) for group A2 than for group A1 tumors. No such subgrouping could be done in B.

TABLE 1

Subgroup	A1						A2					
Tumor position in the cluster	1	2	3	4	5	6	7	8	9	10	11	12
Age, years	46	58	60	63	51	58	46	47	50	47	46	66
Nodal status	1	0	0	16	13	37	10	4	1	2	0	0
Histological size, mm	60	20	26	35	20	30	27	25	30	25	20	22
SBR grade												
ER status	neg	neg	neg	neg	neg	neg	pos	neg	pos	pos	pos	pos
Adjuvant chemotherapy	yes	yes	no	yes	yes	yes	yes	yes	no	yes	no	no
Metastasis	yes	no	yes	yes	no	yes	no	no	no	no	no	no
Follow-up, months	58	106	35	47	41	31	85	98	95	49	19	141
Patient status	D	A	D	D	A	D	A	A	A	A	A	A

Patient characteristics in subgroups A1 and A2. The 12 tumors are numbered from 1 to 12 according to their position from left to right in the clustering graphic displayed in Fig. 3. Adjuvant chemotherapy was anthracyclin-based. In the line concerning the patient status, A means alive and D means death from cancer progression.

Genes responsible for group A substructure were searched. These are potentially relevant to the prognosis and the sensitivity to chemotherapy in these tumors. Thirty-two genes out of 188 were identified by comparing their median expression level in A1 vs A2. Then, the 12 tumors were reclustered using the expression profiles of these genes as shown in Fig. 3. The same subgroups A1 and A2 were evident and separated by 2 groups of genes: as expected, high expression of ERBB2, MYC and EGFR was associated with bad prognosis subgroup A1 (6-8), and that of E-cadherin and the proto-oncogene MYB with good prognosis subgroup A2 (9, 10). For most of the other genes, these results may stimulate new investigations. Differentiation state is a good prognostic factor in breast cancer and, accordingly, genes associated with cell differentiation, such as GATA3 (11) and CRABP2 (12), had a high level of expression in the better outcome group. The high expression of Ephrin-A1 mRNA in the bad prognosis subgroup suggests a role of this growth factor in breast cancer and can be paralleled with its up-regulation during melanoma progression (13).

Differential gene expression between normal breast and breast tumors

To identify genes differentially expressed between breast tumors (T) and normal breast (NB), the NB value for each gene was compared to its expression level in each tumor. When the expression level of a gene in NB was undetectable, only qualitative information could be deduced and the mRNA was considered as differentially expressed if the signal intensity in the tumor was superior to the reproducibility threshold (0.002% of mRNA abundance). In the other cases, differential expression was defined by an at least 2-fold expression difference. Also, the number of

tumors where it was over- or underexpressed was measured. Table 2 shows a list of the top 20 over- and underexpressed genes. For these genes, the T/NB ratio is reported, where T represented their median expression value in the 34 tumors. This ratio ranged from 2.70 (ABCC5) to 17.76 (GATA3) for the overexpressed genes, and from 0.00 (desmin) to 0.29 (APC) for the underexpressed genes.

TABLE 2

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Overexpressed genes				
154343	Granzyme H	GZMH	14q11.2	32	9,51
235947	Stromelysin 3	STMY3	22q11.2	31	15,92
207378	MYB Related Protein B	MYBL2	20q13.1	31	(a)
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	1q21.3	29	7,16
129757	GATA-binding protein 3	GATA3	10p15	28	17,76
120649	T-Lymphocyte surface CD2 antigen	CD2	1p13.1	28	7,54
109677	CREB Binding Protein	CREBBP	16p13.3	28	5,08
172152	EGFR-binding protein GRB2	GRB2	17q24-q25	28	5,00
66969	Transcription factor RELB	RELB	19	28	3,61
182007	ETS-Related Transcription Factor ELF1	ELF1	13q13	27	3,58
153446	LIM domain protein RIL	RIL	5q31.1	26	4,03
203394	ETS Variant gene 5 (ETS-related molecule)	ETV5	3q28	25	3,67
160963	Thrombospondin 1	THBS1	15q15	25	3,39
188393	POU domain, class 2, transcription Factor 2	POU2F2	19	24	4,02

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
187822	Integrin, beta 2	ITGB2	21q22.3	24	3,01
243907	Nuclear Factor of Activating T cell Subunit p45	NF45	1	24	2,84
158347	EST H27202	EST		23	2,91
230933	EST AW184517	EST		22	2,85
212366	ATP-Binding Cassette, sub-family C (CFTR/MRP), 5	ABCC5	3q27	22	2,70
149401	Cathepsin D	CTSD	11p15.5	21	2,97
	Underexpressed genes				
153854	Desmin	DES	2q35	34	0,00
208717	P55-C-FOS proto-oncogene protein	FOS	14q24.3	33	0,05
159093	Transcription Factor AP4	TFAP4	16p13	33	0,11
124340	Tenascin XA	TNXA	6p21.3	33	0,14
133738	Prolactin	PRL	6p22.2-p21.3	32	0,00
133891	Chorionic Somatomammotropin Hormone 1	CSH1	17q22-q24	32	0,00
151501	Tyrosine Kinase Receptor TEK	TEK	9p21	32	0,00
183030	Activating Transcription Factor 3	ATF3	1	32	0,07
120916	Phosphodiesterase I	PDNP2	8q24.1	32	0,14
155716	EST R72075	EST		31	0,00
208118	Transforming Growth Factor Beta Receptor Type III	TGFB3	1p33-p32	31	0,14
187547	Diphtheria Toxin Receptor	DTR	5q23	31	0,17
108490	HIV-1 Rev Binding protein	HRB	2q36	31	0,20
147002	B-cell CLL/lymphoma 2	BCL2	18q21.3	31	0,26
182610	Microsomal Glutathione S Transferase 1	MGST1	12p12.3-p12.1	31	0,28
152802	Phospholipase A2 Membrane	PLA2G2A	1p35	30	0,03

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Associated, group IIA				
183087	Interleukin 3 Receptor Alpha chain	IL3RA	Xp22.3;Yp13.3	30	0,24
108571	Retinoblastoma-Like 2 (p130)	RBL2	16q12.2	29	0,28
125294	Adenomatous Polyposis Coli Protein	APC	5q21-q22	29	0,29
151767	FASL Receptor	TNFRSF6	10q24.1	28	0,27

List of the genes that show the most frequent differential expression between normal breast tissue and 34 breast carcinomas as measured by cDNA array analysis. N indicates the number of tumor samples where the gene is dysregulated (fold change > 2) compared to normal breast tissue. T/NB represents the ratio: median expression level in 34 breast tumors / expression level in normal breast. (a) MYBL2 transcript displayed a median expression level of 0.025% in breast tumors and was undetectable in NB.

High expression of mucin 1, NM23, ERBB2, FGFR1 and FGFR2, MYC, stromelysin3, cathepsin D and downregulation of FOS, APC, RBL2, FAS, BCL2 were found, reflecting what is known about their biology in cancer. GATA3, which codes for a member of the GATA family of zinc finger transcription factors, and CRABP2, encoding one of the two cellular retinoic acid-binding proteins, showed high expression of mRNA, extending previous results on cDNA arrays (4).

Differential gene expression among various breast tumors and correlation with histoclinical prognostic parameters

To search for potential prognostic markers in breast cancer, genes with expression levels correlated with conventional histoclinical prognostic parameters were looked for: age of patients, axillary node status, tumor size, histological grade and ER status. No significant correlation was found with age, tumor size and histological grade. However, the expression profiles of some genes correlated with ER status and axillary node involvement.

To identify genes potentially relevant to the hormone-responsive phenotype, the gene expression profiles in ER-positive breast cancers (n = 23) vs ER-negative breast cancers (n = 11) were compared. Sixteen clones displayed a median intensity of 0 in both groups. Twenty-five presented a fold change superior to 2. Table 3a displays the top 10 over- and underexpressed genes. Among them, the most differentially expressed was GATA3 with a median intensity ratio ER+/ER- of 28.6 and a value for the first quartile of ER-positive tumors superior (5-fold) to the value of the third quartile of the ER-negative tumors as shown in Fig. 4a. The high expression of GATA3 in ER-positive tumors was statistically significant using a Mann-Witney test (p 0.001). All ER-positive tumors and only 18% of ER-negative tumors displayed a GATA3 expression level greatly superior (fold change > 3) to the normal breast value. Furthermore GATA3 expression was analyzed by Northern blot hybridization (Fig. 4b) in a panel of 79 breast cancers (21 ER-negative tumors and 58 ER-positive tumors), including 22 of the tumors analyzed with cDNA arrays. It confirmed the array results for those 22 tumors as well as the strong correlation between ER status and GATA3 RNA expression (Mann-Witney test, p ≤ 0.0001).

TABLE 3A

Clone ID	Gene/Protein identity	Gene symbol	ER+/ER-
129757	GATA-binding protein 3	GATA3	28,6
356763	Granzyme A	GZMA	5,7
248613	MYB proto-oncogene	MYB	3,4
211999	KIAA1075 protein	KIAA1075	3,3
235947	Stromelysin 3	STMY3	3,1
229839	Macrophage Stimulating 1	MST1	2,8
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	2,7
301950	X-box Binding Protein 1	XBP1	2,7
205314	Tumor Protein p53	TP53	2,5
126233	Insulin-like Growth Factor 2	IGF2	2,4
66322	CD3G antigen, Gamma	CD3G	0,0
195022	Interleukin 2 Receptor Gamma chain	IL2RG	0,0
111461	SOX4 Protein	SOX4	0,4
151475	Epidermal Growth Factor Receptor	EGFR	0,5
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,5
130788	Topoisomerase (DNA) II beta (180kD)	TOP2B	0,6
323948	SOX9 Protein	SOX9	0,6
183641	S100 calcium-binding protein Beta	S100B	0,6
246620	EST N53133	EST	0,6
231424	Glutathione S Transferase Pi	GSTP1	0,6

To search for genes whose expression profile was correlated with axillary lymph node status, a strong prognostic factor in breast cancer, the group of node-negative tumors (n = 19) was compared with the group of tumors with massive axillary extension (10 or more positive nodes). Furthermore, because survival decreases with the increase of the number of tumor-involved lymph nodes and because the expression measurements were quantitative, it was looked for a correlation between the expression levels of

these genes and the number of tumor-involved nodes (quantitative variables). Table 3b shows a list of the top 10 over- and underexpressed genes between these 2 groups. Most of these genes have not been previously reported as associated with node status, but some of these results are in agreement with literature data. The gene encoding the tyrosine kinase receptor ERBB2 was the most significantly overexpressed gene in node-positive tumors and displayed the highest correlation coefficient ($r = 0.68$; $p \leq 0.0001$).

TABLE 3B

Clone ID	Gene/Protein identity	Gene symbol	N-/10N+
129757	GATA-binding protein 3	GATA3	11,0
160963	Thrombospondin 1	THBS1	6,6
151475	Epidermal Growth Factor Receptor	EGFR	5,4
120916	Phosphodiesterase I	PDNP2	4,9
183030	Activating Transcription Factor 3	ATF3	4,6
211999	KIAA1075 protein	KIAA1075	4,5
110480	Nuclear Factor 1 A-type	NF1A	4,5
182264	P-Selectin	SELP	4,4
356763	Granzyme A	GZMA	4,3
214008	E-cadherin	CDH1	4,0
147016	ERBB2 Receptor Protein-Tyrosine Kinase	ERBB2	0,2
179197	Protein Phosphatase PP2A, 55 kD Subunit	PP2A BR gamma	0,2
231424	Glutathione S Transferase Pi	GSTP1	0,4
111461	SOX4 Protein	SOX4	0,4
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,4
220451	Zinc Finger protein 144	ZNF144	0,5
125413	Mucin 1	MUC1	0,6
290007	CD44 antigen, epithelial form	CD44	0,6
108571	Retinoblastoma-Like 2 (p130)	RBL2	0,7
130788	Topoisomerase (DNA) II Beta (180kD)	TOP2B	0,7

Gene clusters

Gene clustering from Fig. 2b showed groups of genes with correlated expression across samples. When different clones represented the same gene, they were

clustered next to each other (red arrows). Correlation coefficients between gene pairs in the 34 tumors were often high (1% of the 13,041 gene pairs showed a correlation coefficient superior to 0.95 - not shown). An example of highly correlated gene expression is that of BCL2 and RBL2. Such correlated expression, although it has not been described in the literature, probably reflects a common mechanism of regulation for these two genes. Furthermore, these genes also exhibited significant correlated expression with other genes such as PPP2CA, AKT2, PRKCSH or TNFRSF6/FAS. In particular, a striking correlated expression between BCL2 and FAS could be observed ($r = 0.91$; data not shown). The exact meaning of this correlation is unknown, although it may reflect the necessary balance between apoptosis and anti-apoptosis for cell survival.

Although in human cancer the proportion of changes that is reflected at the RNA level is not known, monitoring gene expression patterns appears as a very promising way of increasing the knowledge of the disease. Several different types of cancer have been investigated using cDNA arrays: cervical (14), hepatocellular (15), ovarian (16), colon (17) and renal carcinomas (18), glioblastomas (19), melanomas (20) (21), rhabdomyosarcomas (22), acute leukemias (23) and lymphomas (24). In breast cancer, pioneering studies have yielded the first expression patterns (4, 25-31). They have in particular addressed the important issue of molecular differences in hormone responsive and non-responsive breast tumors. Thus, Yang et al. (28) and Hoch et al. (25) compared expression profiles of breast carcinoma cell lines known to represent these two categories and identified a few genes with differential expression. One of these genes was GATA3. In these studies, cell lines were mostly used and tumor samples were rarely

tested and generally in small numbers. The first study analyzing the expression profiles of a large series of breast cancers was published recently (32), but no correlation with clinical outcome was mentioned.

5 Several interesting points can be made based on the present experimentation. First, the differences in expression patterns among the tumors provided molecular transcriptional evidence of the histoclinical heterogeneity of breast cancer. This diversity was multifactorial, linked
10 to many different genes, highlighting the interest of high throughput analysis in this context. It was possible, with a hierarchical clustering program integrating the expression profiles, to separate normal breast tissue from most tumors and, moreover, to identify two different groups of tumors.
15 Most importantly, two different subgroups of tumors with a very distinct clinical outcome that could not be predicted with classical prognostic factors have been identified by clustering. Indeed, all these tumors had a theoretically bad prognosis as evaluated by current histoclinical tools. All
20 these patients would be at the present time treated with adjuvant chemotherapy, but without the capacity for the physicians to identify patients who will benefit of this treatment and those who will not benefit.

Gene expression profiles were able to make this
25 discrimination. Such predictive tools have important therapeutic implications. Patients with features of poor prognosis are candidates for other treatment than standard chemotherapy, avoiding loss of time and toxicities related to first-line chemotherapy. These results suggest that the
30 histoclinical category of poor prognosis breast cancer, currently treated with adjuvant anthracyclin-based chemotherapy, groups together at least two molecularly distinct subgroups of tumors with different outcome which

would require distinct chemotherapy regimens. Expression profiles could thus provide a new and more accurate way of classifying breast tumors of poor prognosis and managing patients.

5 Similarly, despite molecular heterogeneity, significant correlations between the expression level of genes (GATA3, ERBB2) and histological tumor parameters were identified. The ER-positivity in breast cancer has been correlated with tumor differentiation, low proliferating
10 rate, favorable prognosis and response to hormonal therapy. The relation between hormone sensitivity of breast cancer and ER status is not perfect, and it is possible that some genes related to ER expression are more important than ER to characterize the hormone sensitive phenotype. These genes
15 could serve as predictive factors to guide the therapy.

 GATA3 mRNA expression was highly correlated with ER status. GATA3, which is not estrogen-regulated (25), is a transcription factor that could regulate the expression of genes involved in the ER-positive phenotype. Among the other
20 genes that were found associated with ER status during the experimental work leading to the present invention, some, such as MYB (10), stromelysin 3 (33), and CRABP2 (34), have been previously reported expressed at high levels in ER-positive breast tumors. The higher levels of TP53 mRNA in
25 ER-positive tumors studied were surprising, although in agreement with a recent study (27). Most studies concerning TP53 expression analyzed the protein level rather than the mRNA level, and TP53 protein levels are classically negatively correlated with the ER status (35). The high
30 expression of CRABP2 could be related to the better differentiated status of the ER-positive tumors. The low expression of the three immunity-related genes IL2RB, IL2RG and CD3G may be related to the low lymphoid infiltration in

these well differentiated tumors. ERBB2 high expression in breast cancer has been associated with a poor prognosis and some resistance to hormonal therapy and chemotherapy (36). It is involved in the regulation of cellular differentiation, adhesion, and motility. The motility-enhancing activity of ERBB2 (37) could be responsible for the increased metastatic potential and the unfavorable prognosis of the breast tumors that overexpress ERBB2. The low expression of E-cadherin and thrombospondin 1 in node-positive tumors are consistent with their putative role in different steps of metastatic spread: E-cadherin is an epithelial cell adhesion molecule whose disturbance is a prerequisite for the release of invasive cells in carcinomas (38) and thrombospondin 1 inhibits angiogenesis (39). Similarly, the high expression of the molecule surface antigen Mucin 1 in node-positive tumors (40) can reduce cell-cell interactions facilitating cell detachment and metastasis. CD44, encoding a transmembrane glycoprotein involved in cell adhesion and lymph node homing (41) was expressed at high levels in node-positive tumors as well as GSTP1 (Glutathione-S-Transferase Pi), recently reported associated with increased tumor size (27).

Second, there were a number of genes with highly correlated expression patterns. Gene correlations have already been reported with larger series of genes, essentially under dynamic experimental conditions (42) and recently in steady states (17). Here, correlations were based on expression profiles of a relatively small but selected series of genes and in steady states represented by different breast tumors. Gene correlations are potentially useful tools for cancer research in two ways: i)- they can provide information about the general regulation circuitry of a cancerous cell, allowing the identification of regulatory elements controlling expression networks; ii)- they offer the

possibility of reducing the complexity of the system analyzed by replacing, for example, the intensities of a large number of genes present in a gene cluster by their respective mean intensities.

5 Finally, these results highlight the great potential of cDNA array in cancer research. The gene expression profiles confirmed the heterogeneity of breast cancer, and most importantly allowed us to identify, among a series of poor prognosis breast tumors, two subtypes of the
10 disease not yet recognized with usual histoclinical parameters but with a different clinical outcome after adjuvant chemotherapy. Furthermore, the present invention allows detecting genes of which expression was correlated with classical prognostic factors.

15 Table 4 displays a library of polynucleotides SEQ ID NO :1 to SEQ ID NO : 468 corresponding to a population of polynucleotide sequences underexpressed or overexpressed in cells derived from tumors, more particularly breast tumors,
20 and their respective complements.

TABLE 4

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
HRB	1	hiv-1 rev binding protein	SEQ ID No:1		SEQ ID No:2
GATA1	2	gata-binding protein 1 (globin transcription factor 1)		SEQ ID No:3	SEQ ID No:4
TLK2	3	tousled-like kinase 2		SEQ ID No:5	SEQ ID No:6
EST T81919	4	ests, weakly similar to alu7_human alu subfamily sq sequence contamination warning entry [h.sapiens]	SEQ ID No:7	SEQ ID No:8	
CCND1	5	cyclin d1 (prad1: parathyroid adenomatosis 1)	SEQ ID No:9		SEQ ID No:10
STAT1	6	signal transducer and activator of transcription 1, 91kd		SEQ ID No:11	SEQ ID No:12
FGFR2	7	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome)	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
EST T89980	8	ests	SEQ ID No:16		
PPP3CC	9	protein phosphatase 3 (formerly 2b), catalytic subunit, gamma isoform (calcineurin a gamma)	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
EST T90726	10	ests	SEQ ID No:20	SEQ ID No:21	
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
RNF5	12	ring finger protein 5		SEQ ID No:25	SEQ ID No:26
AXL	13	axl receptor tyrosine kinase	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
PPP4C	15	protein phosphatase 4 (formerly x), catalytic subunit	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EST T79867	16	ests	SEQ ID No:35		
FGFR4	17	fibroblast growth factor receptor 4	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(autotaxin)			
RELA	19	v-rel avian reticuloendotheliosis viral oncogene homolog a (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3 (p65))	SEQ ID No:42		SEQ ID No:43
ITK	20	il2-inducible t-cell kinase		SEQ ID No:44	SEQ ID No:45
TNXB	21	tenascin xb		SEQ ID No:46	SEQ ID No:47
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
APC	24	adenomatosis polyposis coli	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
SYK	29	spleen tyrosine kinase	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
IL7R	30	interleukin 7 receptor		SEQ ID No:71	SEQ ID No:72
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GRB7	33	growth factor receptor-bound protein 7	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
CASP4	35	caspase 4, apoptosis-related cysteine protease	SEQ ID No:84		SEQ ID No:85
TIMP2	36	tissue inhibitor of metalloproteinase 2		SEQ ID No:86	SEQ ID No:87
DDT	37	d-dopachrome tautomerase	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
PRL	38	prolactin	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:91	No:92	No:93
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
PGF	42	placental growth factor, vascular endothelial growth factor-related protein		SEQ ID No:102	SEQ ID No:103
UBE3A	43	ubiquitin protein ligase e3a (human papilloma virus e6-associated protein, angelman syndrome)		SEQ ID No:104	SEQ ID No:105
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
TIE	45	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains		SEQ ID No:109	SEQ ID No:110
AMFR	46	autocrine motility factor receptor	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
EST R81127	47	homo sapiens mrna; cdna dkfzp434c136 (from clone dkfzp434c136)	SEQ ID No:114		
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
MDM2	50	mouse double minute 2, human homolog of; p53-binding protein		SEQ ID No:120	SEQ ID No:121
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
HIP-55	52	src homology 3 domain-containing protein hip-55	SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
CTSD	53	cathepsin d (lysosomal aspartyl protease)	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
IGF1R	54	insulin-like growth factor 1 receptor		SEQ ID No:129	SEQ ID No:130
INSR	55	insulin receptor		SEQ ID No:131	SEQ ID No:132
FOXO1A	56	forkhead box o1a (rhabdomyosarcoma)		SEQ ID No:133	SEQ ID No:134
EGFR	57	epidermal growth factor receptor	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	No:135	No:136	No:137
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
TNFRSF6	59	tumor necrosis factor receptor superfamily, member 6	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CDKN1A	60	cyclin-dependent kinase inhibitor 1a (p21, cip1)	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
GAPD	62	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
JUNB	63	jun b proto-oncogene	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ACVRL1	65	activin a receptor type ii-like 1	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
RIL	66	lim domain protein		SEQ ID No:162	SEQ ID No:163
SHC1	67	shc (src homology 2 domain-containing) transforming protein 1		SEQ ID No:164	SEQ ID No:165
GAPD	68	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
CSNK2B	70	casein kinase 2, beta polypeptide		SEQ ID No:171	SEQ ID No:172
GLG1	71	golgi apparatus protein 1	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
EDNRB	72	endothelin receptor type b		SEQ ID No:176	SEQ ID No:177
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
FGFR1	74	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome)	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
PPP2CA	75	protein phosphatase 2 (formerly 2a), catalytic subunit, alpha isoform		SEQ ID No:183	SEQ ID No:184
EST R55460	76	homo sapiens, clone image:4054156, mRNA, partial cds		SEQ ID No:185	

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
MC1R	78	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)		SEQ ID No:187	SEQ ID No:188
NRG1	79	neuregulin 1	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
CNTFR	80	ciliary neurotrophic factor receptor		SEQ ID No:192	SEQ ID No:193
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
ENG	82	endoglin (osler-rendu-weber syndrome 1)	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
HRMT1L1	84	hmt1 (hmrnp methyltransferase, s. cerevisiae)-like 1	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
ETV4	85	ets variant gene 4 (ela enhancer-binding protein, elaf)	SEQ ID No:204	SEQ ID No:205	
ANXA11	86	annexin a11		SEQ ID No:206	SEQ ID No:207
PDGFRB	87	platelet-derived growth factor receptor, beta polypeptide		SEQ ID No:208	SEQ ID No:209
WBSCR14	88	williams-beuren syndrome chromosome region 14		SEQ ID No:210	SEQ ID No:211
CD74	89	cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated)		SEQ ID No:212	SEQ ID No:213
ANXA7	90	annexin a7		SEQ ID No:214	SEQ ID No:215
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PTPN2	92	protein tyrosine phosphatase, non-receptor type 2	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
EPHA2	93	epha2	SEQ ID No:221		SEQ ID No:222
TIMP1	94	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
GRB2	97	growth factor receptor-bound protein 2	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
JUND	98	jun d proto-oncogene	SEQ ID No:233		SEQ ID No:234
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
THBS3	101	thrombospondin 3	SEQ ID No:240		SEQ ID No:241
ACTG1	102	actin, gamma 1	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	103	integrin, alpha 6	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
RAD9	104	rad9 (s. pombe) homolog	SEQ ID No:248		SEQ ID No:249
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
AKT2	106	v-akt murine thymoma viral oncogene homolog 2	SEQ ID No:253		SEQ ID No:254
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
SELE	109	selectin e (endothelial adhesion molecule 1)	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
PRKCSH	111	protein kinase c substrate 80k-h		SEQ ID No:263	SEQ ID No:264
DTR	112	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)		SEQ ID No:265	SEQ ID No:266
ITGB2	113	integrin, beta 2 (antigen cd18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)		SEQ ID No:267	SEQ ID No:268
NEO1	114	neogenin (chicken) homolog 1		SEQ ID No:269	SEQ ID No:270
POU2F2	115	pou domain, class 2, transcription	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		factor 2	No:271		No:272
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
PTK2	121	ptk2 protein tyrosine kinase 2		SEQ ID No:284	SEQ ID No:285
CDK4	122	cyclin-dependent kinase 4	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
BTF3	123	basic transcription factor 3	SEQ ID No:289		SEQ ID No:290
CSF1R	124	colony stimulating factor 1 receptor, formerly mcdonough feline sarcoma viral (v-fms) oncogene homolog	SEQ ID No:291		SEQ ID No:292
FLI1	125	friend leukemia virus integration 1	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
ETV5	127	ets variant gene 5 (ets-related molecule)	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4	128	cyclin-dependent kinase 4	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
YES1	129	v-yes-1 yamaguchi sarcoma viral oncogene homolog 1	SEQ ID No:303		SEQ ID No:304
IFI75	130	interferon-induced protein 75, 52kd	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
TGFBR3	132	transforming growth factor, beta receptor iii (betaglycan, 300kd)	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
PRDX2	133	peroxiredoxin 2	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
FOS	134	v-fos fbj murine osteosarcoma viral oncogene homolog		SEQ ID No:317	SEQ ID No:318

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RBBP7	135	retinoblastoma-binding protein 7	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
KIAA107 5	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
ABCC5	137	atp-binding cassette, sub-family c (cftr/mrp), member 5		SEQ ID No:324	SEQ ID No:325
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
PCNA	143	proliferating cell nuclear antigen	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MGC1307 1	146	hypothetical protein mgc13071	SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
ILF2	147	interleukin enhancer binding factor 2, 45kd		SEQ ID No:350	SEQ ID No:351
FLJ1130 7	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
ZNF9	150	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	SEQ ID No:356		SEQ ID No:357
CREM	151	camp responsive element modulator	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
ETV5	155	ets variant gene 5 (ets-related	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		molecule)	No:368	No:369	No:300
CD69	156	cd69 antigen (p60, early t-cell activation antigen)		SEQ ID No:370	SEQ ID No:371
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
MXI1	160	max-interacting protein 1		SEQ ID No:380	SEQ ID No:381
HOXA5	161	homeo box a5	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TNFAIP3	163	tumor necrosis factor, alpha-induced protein 3	SEQ ID No:388	SEQ ID No:389	SEQ ID No:390
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
FOS	170	v-fos fbj murine osteosarcoma viral oncogene homolog	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RELB	175	v-rel avian reticuloendotheliosis viral oncogene homolog b (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3)	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1)	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	
ESTs H42957 & H42888	187	Human interleukin 3 receptor (hIL-3Ra)	SEQ ID No:440	SEQ ID No:441	
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442	SEQ ID No:443	
ERBB2	189	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	SEQ ID No:444		
ZNF144	190	zinc finger protein 144 (Mel-18) (ZNF144)	SEQ ID No:445		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
MARK3	191	MAP/microtubule affinity-regulating kinase 3 (MARK3)	SEQ ID No:446	SEQ ID No:447	
EST N68536	192	EST N68536 MAX-interacting protein 1 (MXI1)	SEQ ID No:448		
EST R81126	193	EST R81126 lymphotoxin beta receptor (LTBR)		SEQ ID No:449	
POU2F2	194	(POU2F2)		SEQ ID No:450	
CASP1	195	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)		SEQ ID No:451	
HRB	196	syndecan 1 (SDC1) (ex HRB)		SEQ ID No:452	
ITGB2	197	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	SEQ ID No:453		
MGST1	198	protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)		SEQ ID No:454	
PPP2CA	199	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	SEQ ID No:455		
SUI1	200	S100 calcium-binding protein A11 (calgizzarin) (S100A11)		SEQ ID No:456	
GZMA	201	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)		SEQ ID No:457	
EDN1	202	endothelin 1 (EDN1)	SEQ ID No:458		
PTPN6	203	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	SEQ ID No:459		
TFAP4	204	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)	SEQ ID No:460		
CCND2	205	cyclin D2 (CCND2)	SEQ ID No:461		
JUP	206	junction plakoglobin (JUP)	SEQ ID No:462		
GADD45A	207	growth arrest and DNA-damage-inducible, alpha (GADD45A)	SEQ ID No:463		
nm23	208	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	SEQ ID No:464		
BBC1	209	ribosomal protein L13 (RPL13) (ex	SEQ ID		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		BBC1)	No:465		
VEGFB	210	vascular endothelial growth factor B (VEGFB)	SEQ ID No:466		
LAMR1	211	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	SEQ ID No:467		
CSH1	212	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor		SEQ ID No:468	

Tables 5A and 5B hereunder displays two subpopulations corresponding to the 5 top overexpressed and to the 5 top underexpressed polynucleotide sequences particularly interesting to distinguish healthy person from cancer patient.

TABLE 5A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		

TABLE 5B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
PRL	38	prolactin	SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		

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Table 6 hereunder relate to sub populations of polynucleotide sequences interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples.

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TABLE 6

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
MMP11	145	matrix metalloproteinase (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442		

Tables 6A et 6B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples

Table 6A
overexpressed genes : top 5
ER + / ER -

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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Table 6B
underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 7 hereunder relates to subpopulations of polynucleotide sequences interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T89980	8	ests	SEQ ID No:16		
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	

Tables 7A and 7B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors with lymph node from tumors with no lymph node.

TABLE 7A

Overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252

TABLE 7B

Underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336

5 Tables 8, 8A and 8B hereunder relates to sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLE 8

A1 /A2

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	

Tables 8A and 8B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLEAU 8A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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TABLEAU 8B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 9, 9A and 9B hereunder relates to sub populations of polynucleotide sequences particularly interesting in classifying good and poor prognosis primary breast tumors.

TABLE 9

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:275		No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
BS69	144	adenovirus 5 e1a binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		cephalopolysyndactyly syndrome)			
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9A

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
BS69	144	adenovirus 5 e1a binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDI A	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9B

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
EST W73386	168	ests	SEQ ID No:401		

Overexpression of genes detected by using at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A combined with underexpression of genes detected with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B present a Good outcome.

So, a preferred DNA array according to the invention comprises at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A and at least

one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B.

5 Such DNA arrays are particularly useful to distinguish patients having a high risk (Bad Outcome) from those having a good pronostic (Good Outcome).

TABLE 10

CORRELATION BETWEEN SEQ ID NO AS FILED WITH US PROVISIONAL APPLICATION N° 60/254,090
and SEQ ID NO FILED WITH PCT APPLICATION

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
GATA3	1	GATA-binding protein 3 (GATA3)	129757	SEQ ID No : 1		SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
MYB	2	v-myb avian myeloblastosis viral oncogene homolog (MYB)	248613		SEQ ID No : 2	0	SEQ ID No:354	SEQ ID No:355
KIAA1075	3	KIAA1075 protein	211999	SEQ ID No : 3	SEQ ID No : 4	SEQ ID No:322	SEQ ID No:323	0
STMV3	4	matrix metalloproteinase 11 (stromelysin 3) (MMP11) (ex STMV3)	235947	SEQ ID No : 5		SEQ ID No:345	0	SEQ ID No:346
HGFL	5	macrophage-stimulating protein (MST1) (ex HGFL)	229839	SEQ ID No : 6	SEQ ID No : 7	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
CRABP	6	cellular retinoic acid-binding protein 2 (CRABP2)	153275	SEQ ID No : 8	SEQ ID No : 9	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
XBP1	7	X-box binding protein 1 (XBP1)	301950	SEQ ID No : 10	SEQ ID No : 11	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TP53	8	tumor protein p53 (LI-Fraumeni syndrome) (TP53)	205314		SEQ ID No : 12	SEQ ID No:442	0	0
IGF2	9	insulin-like growth factor 2 (somatomedin A) (IGF2)	126233	SEQ ID No : 13	SEQ ID No : 14	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
CD3G	10	CD3G antigen, gamma polypeptide (T1T3 complex) (CD3G)	66322	SEQ ID No : 15	SEQ ID No : 16	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
IL2RG	11	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG)	195022	SEQ ID No : 17	SEQ ID No : 18	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
SOX4	12	SRY (sex determining region Y)-box 4 (SOX4)	111461	SEQ ID No : 19	SEQ ID No : 20	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
EGFR	13	epidermal growth factor receptor (avian erythroblastic)	151475	SEQ ID No : 21	SEQ ID No : 22	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
TOP2B	14	topoIIb mRNA for topoisomerase IIb.	130788		SEQ ID No : 23	0	SEQ ID No:82	SEQ ID No:83
S100B	15	S100 calcium-binding protein, beta (neural) (S100B)	183641		SEQ ID No : 24	0	SEQ ID No:255	SEQ ID No:256
EST N53133	16	EST N53133	246620	SEQ ID No : 25		SEQ ID No:352	0	SEQ ID No:353
GSTP1	17	glutathione S-transferase pI (GSTP1)	231424	SEQ ID No : 26	SEQ ID No : 27	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
THBS1	18	thrombospondin 1 (THBS1)	160963	SEQ ID No : 28		SEQ ID No:216	0	SEQ ID No:217

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
PDPN2	19	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autolysin) (ENPP2) (ex PDPN2)	120916	SEQ ID No : 29	SEQ ID No : 30	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
ATF3	20	activating transcription factor 3 (ATF3)	183030	SEQ ID No : 31	SEQ ID No : 32	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
NF1A	21	(ex NF1A)	110480	SEQ ID No : 33		SEQ ID No:16	0	0
SELP	22	selectin P (granule membrane protein 140kD, antigen CD62) (SELP)	182264		SEQ ID No : 34	SEQ ID No:438	SEQ ID No:439	0
CDH1	23	cadherin 1, E-cadherin (epithelial) (CDH1)	214008	SEQ ID No : 35	SEQ ID No : 36	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ERBB2	24	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	147016	SEQ ID No : 37		0	SEQ ID No:118	SEQ ID No:119
PP2A BR gamma	25	(PP2A BR gamma)	179197	SEQ ID No : 38	SEQ ID No : 39	SEQ ID No:238	SEQ ID No:239	0
ZNF144	26	zinc finger protein 144 (Mel-18) (ZNF144)	220451	SEQ ID No : 40	SEQ ID No : 41	0	SEQ ID No:329	SEQ ID No:330
MUC1	27	mucin 1, transmembrane (MUC1)	125413		SEQ ID No : 42	0	SEQ ID No:57	SEQ ID No:58
CD44	28	CD44E (epithelial form)	290007	SEQ ID No : 43	SEQ ID No : 44	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
PLA2G2A	29	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein	152802	SEQ ID No : 45	SEQ ID No : 46	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
ACVRL1	30	activin A receptor type II-like 1 (ACVRL1)	153350	SEQ ID No : 47	SEQ ID No : 48	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
AXL	31	AXL receptor tyrosine kinase (AXL)	112500	SEQ ID No : 49	SEQ ID No : 50	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
PKU-ALPHA	32	KU-alpha, partial cds (new gene symbol Tik2)	109569		SEQ ID No : 51	0	SEQ ID No:5	SEQ ID No:6
ABCC5	33	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	212366		SEQ ID No : 52	0	SEQ ID No:324	SEQ ID No:325
EDNRB	34	endothelin receptor type B (EDNRB), transcript variant1	154244		SEQ ID No : 53	0	SEQ ID No:176	SEQ ID No:177
DTR	35	diphtheria toxin receptor (heparin-binding epidermal)	187547		SEQ ID No : 54	0	SEQ ID No:265	SEQ ID No:266
IGF1R	36	insulin-like growth factor 1 receptor (IGF1R)	150361		SEQ ID No : 55	0	SEQ ID No:129	SEQ ID No:130
KIAA0427	37	KIAA0427	127507	SEQ ID No : 56	SEQ ID No : 57	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
CD69	38	CD69 antigen (p60, early T-cell activation antigen)	276727		SEQ ID No : 58	0	SEQ ID No:370	SEQ ID No:371
FGFR4	39	fibroblast growth factor receptor 4 (FGFR4)	116781	SEQ ID No : 59	SEQ ID No : 60	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
EST T85683	40	EST T85683 cathepsin B (CTSB)	112622		SEQ ID No : 61	0	SEQ ID No:30	SEQ ID No:31
EST R00569	41	EST R00569 IL2-inducible T-cell kinase (ITK)	123871		SEQ ID No : 62	0	SEQ ID No:44	SEQ ID No:45

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TGFR3	42	transforming growth factor, beta receptor III (TGFR3)	208118	SEQ ID No : 63	SEQ ID No : 64	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
INSR	43	insulin receptor (INSR)	151149		SEQ ID No : 65	0	SEQ ID No:131	SEQ ID No:132
MARK3	44	MAP/microtubule affinity-regulating kinase 3 (MARK3)	110599	SEQ ID No : 66	SEQ ID No : 67	#N/A	#N/A	#N/A
TIMP2	45	tissue inhibitor of metalloproteinase 2 (TIMP2)	131504		SEQ ID No : 68	0	SEQ ID No:86	SEQ ID No:87
EST R85557	46	EST R85557 thrombospondin 3 (THBS3)	180219	SEQ ID No : 69		SEQ ID No:240	0	SEQ ID No:241
GNRH1	47	gonadotropin-releasing hormone 1 (GNRH1)	192688		SEQ ID No : 70	0	SEQ ID No:277	SEQ ID No:278
FGFR2	48	fibroblast growth factor receptor 2 (FGFR2)	110387	SEQ ID No : 71	SEQ ID No : 72	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
NFKB2	49	NFKB2	114879	SEQ ID No : 73		SEQ ID No:35	0	0
VIL2	50	villin 2 (ezrin) (VIL2)	124701	SEQ ID No : 74	SEQ ID No : 75	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
ENG	51	endoglin (ENG)	156979	SEQ ID No : 76	SEQ ID No : 77	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EPHA2	52	Epha2 (EPHA2)	162004	SEQ ID No : 78		SEQ ID No:221	0	SEQ ID No:222
CREM	53	cAMP responsive element modulator (CREM)	258584	SEQ ID No : 79	SEQ ID No : 80	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
ETV5-a	54	ets variant gene 5 (ETV5)	270549	SEQ ID No : 81	SEQ ID No : 82	SEQ ID No:368	SEQ ID No:369	SEQ ID No:300
EST N68536	55	EST N68536 MAX-interacting protein 1 (MXI1)	298242	SEQ ID No : 83	SEQ ID No : 84	0	SEQ ID No:380	SEQ ID No:381
EST R81126	56	EST R81126 lymphotoxin beta receptor (LTBR)	146635	SEQ ID No : 85	SEQ ID No : 86	SEQ ID No:114	0	0
POU2F2	57	POU2F2	188393	SEQ ID No : 87	SEQ ID No : 88	SEQ ID No:271	0	SEQ ID No:272
FLI1	58	Friend leukemia virus integration 1 (FLI1)	198144	SEQ ID No : 89	SEQ ID No : 90	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
TIE	59	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE)	144081		SEQ ID No : 91	0	SEQ ID No:109	SEQ ID No:110
PRLR	60	prolactin receptor (PRLR)	138788	SEQ ID No : 92	SEQ ID No : 93	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
PPP3CA	61	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC) (ex PPP3CA)	110481	SEQ ID No : 94	SEQ ID No : 95	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
PTPN2	62	protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	161451	SEQ ID No : 96	SEQ ID No : 97	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
PGF	63	placental growth factor, vascular endothelial growth factor-related protein (PGF)	139326		SEQ ID No : 98	0	SEQ ID No:102	SEQ ID No:103
TNFAIP3	64	tumor necrosis factor, alpha-induced	309943	SEQ ID No : 99		SEQ ID No:388	SEQ ID No:389	SEQ ID No:390

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		protein 3 (TNFAIP3)						
PHB	65	PHB (prohibitin)	236008	SEQ ID No : 100		SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
RIL	66	LIM domain protein (RIL)	153446		SEQ ID No : 101	0	SEQ ID No:162	SEQ ID No:163
MYBL2	67	v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2)	207378	SEQ ID No : 102	SEQ ID No : 103	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
RELB	68	v-rel avian reticuloendotheliosis oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB)	66969	SEQ ID No : 104	SEQ ID No : 105	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
EST R97218	69	Est R97218	200394	SEQ ID No : 106		SEQ ID No:296	SEQ ID No:297	0
GZMH	70	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB) (ex GZMH)	154343	SEQ ID No : 107		SEQ ID No:178	0	SEQ ID No:179
MYC	71	c-myc proto-oncogene	129438	SEQ ID No : 108	SEQ ID No : 109	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
CASP1	72	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)	131502		SEQ ID No : 110	SEQ ID No:84	0	SEQ ID No:85
SYK	73	spleen tyrosine kinase (SYK)	128142	SEQ ID No : 111	SEQ ID No : 112	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
EST H27202	74	EST H27202 transcription factor E1AF gene	158347	SEQ ID No : 113	SEQ ID No : 114	SEQ ID No:204	SEQ ID No:205	0
HRB	75	syndecan 1 (SDC1) (ex HRB)	108490	SEQ ID No : 115	SEQ ID No : 116	SEQ ID No:1	0	SEQ ID No:2
SHC1	76	p86shc (SHC)	153548		SEQ ID No : 117	0	SEQ ID No:164	SEQ ID No:165
CSF1	77	colony stimulating factor 1 (CSF1)	124554	SEQ ID No : 118	SEQ ID No : 119	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
UBE3A	78	ubiquitin protein ligase E3A (UBE3A)	141924		SEQ ID No : 120	0	SEQ ID No:104	SEQ ID No:105
FKHR	79	forkhead box O1A (rhabdomyosarcoma) (FOXO1A) (ex FKHR)	151247		SEQ ID No : 121	0	SEQ ID No:133	SEQ ID No:134
CSF1R	80	colony stimulating factor 1 receptor (CSF1R)	196282	SEQ ID No : 122		SEQ ID No:291	0	SEQ ID No:292
IFI75	81	interferon-induced protein 75 (IFI75)	205612	SEQ ID No : 123	SEQ ID No : 124	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
GATA1	82	GATA-binding protein 1 (globin transcription factor 1) (GATA1)	109093		SEQ ID No : 125	0	SEQ ID No:3	SEQ ID No:4
STAT1	83	signal transducer and activator of transcription 1 (STAT1)	110101		SEQ ID No : 126	0	SEQ ID No:11	SEQ ID No:12
CREBBP	84	CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP)	109677	SEQ ID No : 127	SEQ ID No : 128	SEQ ID No:7	SEQ ID No:8	0
IL7R	85	interleukin 7 receptor (IL7R)	129059		SEQ ID No : 129	0	SEQ ID No:71	SEQ ID No:72
ANXA7	86	annexin A7 (ANXA7)	160580		SEQ ID No : 130	0	SEQ ID No:214	SEQ ID No:215

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TNXA	87	tenascin XA (TNXA)	124340		SEQ ID No : 131	0	SEQ ID No:46	SEQ ID No:47
CNBP1	88	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9) (ex CNBP1)	251963	SEQ ID No : 132		SEQ ID No:356	0	SEQ ID No:357
CDK4-a	89	cyclin-dependent kinase 4 (CDK4)	204586	SEQ ID No : 133	SEQ ID No : 134	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
CSNK2B	90	gene for casein kinase II subunit beta (EC 2.7.1.37)	153879		SEQ ID No : 135	0	SEQ ID No:171	SEQ ID No:172
EFNA1	91	ephrin-A1 (EFNA1)	162997		SEQ ID No : 136	0	SEQ ID No:226	SEQ ID No:227
SELE	92	selectin E (endothelial adhesion molecule 1) (SELE)	186132	SEQ ID No : 137	SEQ ID No : 138	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
APC	93	adenomatosis polyposis coli (APC)	125294	SEQ ID No : 139	SEQ ID No : 140	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
FAK	94	PTK2 protein tyrosine kinase 2 (PTK2) (ex FAK)	195731		SEQ ID No : 141	0	SEQ ID No:284	SEQ ID No:285
FOS-a	95	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	208717		SEQ ID No : 142	0	SEQ ID No:317	SEQ ID No:318
FGFR1	96	fibroblast growth factor receptor (FGFR)	154472	SEQ ID No : 143	SEQ ID No : 144	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
MC1R	97	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R)	155691		SEQ ID No : 145	0	SEQ ID No:187	SEQ ID No:188
PCNA	98	proliferating cell nuclear antigen (PCNA)	232941	SEQ ID No : 146	SEQ ID No : 147	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
DDT	99	D-dopachrome tautomerase (DDT)	132109	SEQ ID No : 148	SEQ ID No : 149	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
GRB2	100	growth factor receptor-bound protein 2 (GRB2)	172152	SEQ ID No : 150	SEQ ID No : 151	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
AMFR	101	autocrine motility factor receptor (AMFR)	146280	SEQ ID No : 152	SEQ ID No : 153	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
ITGB2	102	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	187822	SEQ ID No : 154		0	SEQ ID No:267	SEQ ID No:268
JUND	103	jun D proto-oncogene (JUND)	175421	SEQ ID No : 155		SEQ ID No:233	0	SEQ ID No:234
NF45	104	interleukin enhancer binding factor 2 (ILF2) (ex NF45)	243907		SEQ ID No : 156	0	SEQ ID No:350	SEQ ID No:351
PPP4C	105	protein phosphatase 4 (formerly X) (PPP4C)	114097	SEQ ID No : 157	SEQ ID No : 158	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EMS1	106	ATX1 (antioxidant protein 1, yeast homolog 1 (ATOX1) (ex EMS1))	149172	SEQ ID No : 159		SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
BCL2	107	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha	147002	SEQ ID No : 160	SEQ ID No : 161	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
MGST1	108	protein phosphatase 1, catalytic subunit	162610	SEQ ID No : 162	SEQ ID No : 163	SEQ ID No:248	0	SEQ ID No:249

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		alpha isoform (PPP1CA) (ex MGST1)						
PDGFRB	109	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	158976		SEQ ID No : 164	0	SEQ ID No:208	SEQ ID No:209
ANXA11	110	annexin A11 (ANXA11)	158892		SEQ ID No : 165	0	SEQ ID No:206	SEQ ID No:207
GPX1	111	histocompatibility class II antigen gamma chain (CD74) (ex GPX1 Glutathion S transférase)	159809		SEQ ID No : 166	0	SEQ ID No:212	SEQ ID No:213
CFR-1	112	Golgi apparatus protein 1 (GLG1) (ex CFR-1)	153974	SEQ ID No : 167	SEQ ID No : 168	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
BTF3L3	113	basic transcription factor 3 (BTF3)	195889	SEQ ID No : 169		SEQ ID No:289	0	SEQ ID No:290
EST R55460	114	EST R55460	154997		SEQ ID No : 170	0	SEQ ID No:185	0
AKT2	115	v-akt murine thymoma viral oncogene homolog 2 (AKT2)	183552	SEQ ID No : 171		SEQ ID No:253	0	SEQ ID No:254
CDKN1A	116	cyclin-dependent kinase inhibitor (CDKN1A)	152524	SEQ ID No : 172	SEQ ID No : 173	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PPP2CA	117	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	154685	SEQ ID No : 174	SEQ ID No : 175	0	SEQ ID No:183	SEQ ID No:184
MDM2	118	mouse double minute 2, human homolog of p53-binding protein (MDM2), transcript variant MDM2	148052	SEQ ID No : 176		0	SEQ ID No:120	SEQ ID No:121
TNFRSF6	119	tumor necrosis factor receptor superfamily, member 6 (TNFRSF6)	151767	SEQ ID No : 177	SEQ ID No : 178	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CNTFR	120	ciliary neurotrophic factor receptor (CNTFR)	156431		SEQ ID No : 179	0	SEQ ID No:192	SEQ ID No:193
JUNB	121	jun B proto-oncogene (JUNB)	153213	SEQ ID No : 180	SEQ ID No : 181	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CCND1	122	cyclin D1 (PRAD1; parathyroid adenomatosis 1) (CCND1)	110022	SEQ ID No : 182		SEQ ID No:9	0	SEQ ID No:10
TDPX1	123	peroxiredoxin 2 (PRDX2) (ex TDPX1)	208439	SEQ ID No : 183	SEQ ID No : 184	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
GRB7	124	growth factor receptor-bound protein 7 (GRB7)	130323	SEQ ID No : 185	SEQ ID No : 186	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
RBBP7	125	retinoblastoma-binding protein 7 (RBBP7)	210874	SEQ ID No : 187	SEQ ID No : 188	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
TIMP1	126	issue inhibitor of metalloproteinase 1 (thyroid potentiating activity, collagenase inhibitor) (TIMP1)	162246	SEQ ID No : 189	SEQ ID No : 190	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
YES1	127	y-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	204634	SEQ ID No : 191		SEQ ID No:303	0	SEQ ID No:304
RNF5	128	ring finger protein 5 (RNF5)	112098		SEQ ID No : 192	0	SEQ ID No:25	SEQ ID No:26
PRKCSH	129	protein kinase C substrate 80K-H (PRKCSH)	187232		SEQ ID No : 193	0	SEQ ID No:263	SEQ ID No:264

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
CTSD	130	cathepsin D (lysosomal aspartyl protease) (CTSD)	149401	SEQ ID No : 194	SEQ ID No : 195	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
NEO1	131	neogenin (chicken) homolog 1 (NEO1)	188380		SEQ ID No : 196	0	SEQ ID No:269	SEQ ID No:270
GAPD-a	132	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	152847			SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
ACTG1	133	actin, gamma 1 (ACTG1)	182291	SEQ ID No : 197		SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	134	Integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 198	SEQ ID No : 199	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
GAPD-b	135	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	153607	SEQ ID No : 200	SEQ ID No : 201	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
ETV5-b	136	ets variant gene 5 (ets-related molecule) (ETV5)	203394	SEQ ID No : 202	SEQ ID No : 203	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4-b	137	cyclin-dependent kinase 4 (CDK4)	195800	SEQ ID No : 204	SEQ ID No : 205	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
FOS-b	138	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	363796	SEQ ID No : 206	SEQ ID No : 207	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
HOXA5	139	homeobox protein (HOX-1.3) (ex Hox A5)	300564	SEQ ID No : 208	SEQ ID No : 209	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
RELA	140	NF-kappa-B transcription factor p65 DNA binding subunit (ex RELA)	122056	SEQ ID No : 210	SEQ ID No : 211	SEQ ID No:42	0	SEQ ID No:43
SUI1	141	S100 calcium-binding protein A11 (calgizzarin) (S100A11)	155345	SEQ ID No : 212	SEQ ID No : 213	SEQ ID No:186	0	0
ANG	142	angiotensin, ribonuclease, RNase A family, 5 (ANG)	156720		SEQ ID No : 214	0	SEQ ID No:194	SEQ ID No:195
ITGA6	143	Integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 215	SEQ ID No : 216	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
PRMT2	144	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1 (HRMT1L1) (ex PRMT2)	158038	SEQ ID No : 217	SEQ ID No : 218	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
EST R55480	145	EST R55480	154997		SEQ ID No : 219	0	SEQ ID No:185	0
GZMA	146	granzyme A (granzyme 1, cytotoxic T- lymphocyte-associated serine esterase 3) (GZMA)	356763	SEQ ID No : 220	SEQ ID No : 221	SEQ ID No:402	0	SEQ ID No:403
SOX9	147	SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex- reversal) (SOX9)	323948	SEQ ID No : 222		SEQ ID No:394	0	SEQ ID No:395
SRF	148	serum response factor (c-fos serum response element-binding transcription factor) (SRF)	321329	SEQ ID No : 223	SEQ ID No : 224	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
EDN1	149	endothelin 1 (EDN1)	153424	SEQ ID No : 225		#N/A	#N/A	#N/A
PTPN6	150	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	66778	SEQ ID No : 226		#N/A	#N/A	#N/A
TFAP4	151	transcription factor AP-4 (activating)	159093	SEQ ID No : 227		0	SEQ ID No:210	SEQ ID No:211

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		enhancer binding protein 4) (TFAP4)						
ELF1	152	Human cis-acting sequence.Elf-1	182007	SEQ ID No : 228		SEQ ID No:437	0	0
CD2	153	CD2 antigen (p50), sheep red blood cell receptor (CD2)	120649	SEQ ID No : 229		SEQ ID No:431	0	0
CCND2	154	cyclin D2 (CCND2)	175256	SEQ ID No : 230		#N/A	#N/A	#N/A
IL3RA	155	interleukin 3 receptor (hIL-3Ra)	183087	SEQ ID No : 231		SEQ ID No:440	SEQ ID No:441	0
JUP	156	junction plakoglobin (JUP)	157958	SEQ ID No : 232		#N/A	#N/A	#N/A
RBL2	157	retinoblastoma-like 2 (p130) (RBL2)	108571	SEQ ID No : 233		SEQ ID No:430	0	0
HOXA4	158	homeo box A4 (HOXA4)	110731	SEQ ID No : 234		SEQ ID No:20	SEQ ID No:21	0
ACY1	159	aminoacylase 1 (ACY1)	160764	SEQ ID No : 235		SEQ ID No:435	SEQ ID No:436	0
GADD45A	160	growth arrest and DNA-damage-inducible, alpha (GADD45A)	115176	SEQ ID No : 236		#N/A	#N/A	#N/A
nm23	161	non-metastatic cells 1, protein (NM23A) expressed in (NMIE1)	174388	SEQ ID No : 237		#N/A	#N/A	#N/A
BBC1	162	ribosomal protein L13 (RPL13) (ex BBC1)	178317	SEQ ID No : 238		#N/A	#N/A	#N/A
VEGFB	163	vascular endothelial growth factor B (VEGFB)	162499	SEQ ID No : 239		#N/A	#N/A	#N/A
LAMR1	164	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	199837	SEQ ID No : 240		#N/A	#N/A	#N/A
IL2RB	165	interleukin 2 receptor, beta (IL2RB)	139073	SEQ ID No : 241	SEQ ID No : 242	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
DES	166	desmin	153854	SEQ ID No : 243		SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
PRL	167	prolactin	133738	SEQ ID No : 244		SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
CSH1	168	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor	133891		SEQ ID No : 245	SEQ ID No:432	0	0
TEK	169	tyrosine protein kinase receptor	151501	SEQ ID No : 246	SEQ ID No : 247	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
Nrg1	170	neuregulin 1 (EST R72075)	155716	SEQ ID No : 248	SEQ ID No : 249	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
PLAT	rien	pas d'EST ni mRNA	160149			SEQ ID No:433	SEQ ID No:434	0
EST AW184517	rien		Image ?					

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CLAIMS

1. A polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 or the complement thereof.

2. A polynucleotide library according to Claim 1 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in anyone of the following predefined sets :

SET 1: (SEQ ID No:1; SEQ ID No:2); SET 2: (SEQ ID No:3; SEQ ID No:4); SET 3: (SEQ ID No:5; SEQ ID No:6); SET 4: (SEQ ID No:7; SEQ ID No:8); SET 5: (SEQ ID No:9; SEQ ID No:10); SET 6: (SEQ ID No:11; SEQ ID No:12); SET 7: (SEQ ID No:13; SEQ ID No:14; SEQ ID No:15); SET 8: (SEQ ID No:16); SET 9: (SEQ ID No:17; SEQ ID No:18; SEQ ID No:19); SET 10: (SEQ ID No:20; SEQ ID No:21); SET 11: (SEQ ID No:22; SEQ ID No:23; SEQ ID No:24); SET 12: (SEQ ID No:25; SEQ ID No:26); SET 13: (SEQ ID No:27; SEQ ID No:28; SEQ ID No:29); SET 14: (SEQ ID No:30; SEQ ID No:31); SET 15: (SEQ ID No:32; SEQ ID No:33; SEQ ID No:34) ; SET 16 : (SEQ ID No:35) ; SET 17 : (SEQ ID No:36; SEQ ID No:37; SEQ ID No:38) ; SET 18 : (SEQ ID No:39; SEQ ID No:40; SEQ ID No:41) ; SET 19 : (SEQ ID No:42; SEQ ID No:43) ; SET 20 : (SEQ ID No:44; SEQ ID No:45) ; SET 21 : (SEQ ID No:46; SEQ ID No:47) ; SET 22 : (SEQ ID No:48; SEQ ID No:49; SEQ ID No:50) ; SET 23 : (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET 24: (SEQ ID No:54; SEQ ID No:55; SEQ ID No:56) ; SET 25: (SEQ ID No:57; SEQ ID No:58) ; SET 26: (SEQ ID No:59; SEQ ID No:60; SEQ ID No:61) ; SET 27: (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET 28: (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;

SET 29: (SEQ ID No:68; SEQ ID No:69; SEQ ID No:70) ; SET 30: (SEQ ID No:71; SEQ ID No:72) ; SET 31 : (SEQ ID No:73; SEQ ID No:74; SEQ ID No:75) ; SET 32 : (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET 33 : (SEQ ID No:79; SEQ ID No:80; SEQ ID No:81) ; SET 34: (SEQ ID No:82; SEQ ID No:83) ; SET 35: (SEQ ID No:84; SEQ ID No:85) ; SET 36: (SEQ ID No:86; SEQ ID No:87) ; SET 37: (SEQ ID No:88; SEQ ID No:89; SEQ ID No:90) ; SET 38: (SEQ ID No:91; SEQ ID No:92; SEQ ID No:93) ; SET 39: (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET 40: (SEQ ID No:97; SEQ ID No:98; SEQ ID No:99) ; SET 41: (SEQ ID No:100; SEQ ID No:101; SEQ ID No:102) ; SET 42: (SEQ ID No:103; SEQ ID No:104; SEQ ID No:105) ; SET 43: (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET 44: (SEQ ID No:109; SEQ ID No:110) ; SET 45: (SEQ ID No:111; SEQ ID No:112; SEQ ID No:113) ; SET 46: (SEQ ID No:114; SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET 47: (SEQ ID No:118; SEQ ID No:119) ; SET 48: (SEQ ID No:120; SEQ ID No:121) ; SET 49: (SEQ ID No:122; SEQ ID No:123; SEQ ID No:124; SEQ ID No:125) ; SET 50: (SEQ ID No:126; SEQ ID No:127; SEQ ID No:128) ; SET 51: (SEQ ID No:129; SEQ ID No:130) ; SET 52: (SEQ ID No:131; SEQ ID No:132) ; SET 53: (SEQ ID No:133; SEQ ID No:134) ; SET 54: (SEQ ID No:135; SEQ ID No:136; SEQ ID No:137) ; SET 55: (SEQ ID No:138; SEQ ID No:139; SEQ ID No:140) ; SET 56: (SEQ ID No:141; SEQ ID No:142; SEQ ID No:143) ; SET 57: (SEQ ID No:144; SEQ ID No:145; SEQ ID No:146) ; SET 58: (SEQ ID No:147; SEQ ID No:148; SEQ ID No:149) ; SET 59: (SEQ ID No:150; SEQ ID No:151; SEQ ID No:152) ; SET 60: (SEQ ID No:153; SEQ ID No:154; SEQ ID No:155) ; SET 61: (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET 62: (SEQ ID No:159; SEQ ID No:160; SEQ ID No:161) ; SET 63: (SEQ ID No:162; SEQ ID No:163) ; SET 64: (SEQ ID No:164; SEQ ID No:165) ; SET 65: (SEQ ID No:166; SEQ ID No:167; SEQ ID No:168) ; SET 66: (SEQ ID No:169; SEQ ID No:170) ; SET 67: (SEQ ID No:171; SEQ ID No:172) ; SET 68: (SEQ ID No:173; SEQ ID No:174; SEQ ID No:175) ; SET 69: (SEQ ID No:176; SEQ ID No:177) ; SET 70: (SEQ ID No:178; SEQ ID No:179) ; SET 71: (SEQ ID No:180; SEQ ID No:181; SEQ ID No:182) ; SET 72: (SEQ ID No:183; SEQ ID No:184) ; SET 73: (SEQ ID No:185) ; SET 74: (SEQ ID No:186) ; SET 75: (SEQ ID No:187; SEQ ID No:188) ; SET 76: (SEQ ID No:189)

SEQ ID No:190; SEQ ID No:191) ; SET 80: (SEQ ID No:192; SEQ ID
No:193) ; SET 81: (SEQ ID No:194; SEQ ID No:195) ; SET 82: (SEQ ID
No:196; SEQ ID No:197; SEQ ID No:198) ; SET 83: (SEQ ID No:199;
SEQ ID No:200) ; SET 84: (SEQ ID No:201; SEQ ID No:202; SEQ ID
5 No:203) ; SET 85: (SEQ ID No:204; SEQ ID No:205) ; SET 86: (SEQ ID
No:206; SEQ ID No:207) ; SET 87: (SEQ ID No:208; SEQ ID No:209) ;
SET 88: (SEQ ID No:210; SEQ ID No:211) ; SET 89: (SEQ ID No:212;
SEQ ID No:213) ; SET 90: (SEQ ID No:214; SEQ ID No:215) ; SET 91:
10 (SEQ ID No:216; SEQ ID No:217) ; SET 92: (SEQ ID No:218; SEQ ID
No:219; SEQ ID No:220) ; SET 93: (SEQ ID No:221; SEQ ID No:222) ;
SET 94: (SEQ ID No:223; SEQ ID No:224; SEQ ID No:225) ; SET 95:
(SEQ ID No:226; SEQ ID No:227) ; SET 96: (SEQ ID No:228; SEQ ID
No:229) ; SET 97: (SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ;
SET 98: (SEQ ID No:233; SEQ ID No:234) ; SET 99: (SEQ ID No:235;
15 SEQ ID No:236; SEQ ID No:237) ; SET 100: (SEQ ID No:238; SEQ ID
No:239) ; SET 101: (SEQ ID No:240; SEQ ID No:241) ; SET 102: (SEQ
ID No:242; SEQ ID No:243; SEQ ID No:244) ; SET 103: (SEQ ID
No:245; SEQ ID No:246; SEQ ID No:247) ; SET 104: (SEQ ID No:248;
SEQ ID No:249) ; SET 105: (SEQ ID No:250; SEQ ID No:251; SEQ ID
20 No:252) ; SET 106: (SEQ ID No:253; SEQ ID No:254) ; SET 107: (SEQ
ID No:255; SEQ ID No:256) ; SET 108: (SEQ ID No:257; SEQ ID
No:258) ; SET 109: (SEQ ID No:259; SEQ ID No:260; SEQ ID No:261) ;
SET 110: (SEQ ID No:262; SEQ ID No:200) ; SET 111: (SEQ ID No:263;
SEQ ID No:264) ; SET 112: (SEQ ID No:265; SEQ ID No:266) ; SET
25 113: (SEQ ID No:267; SEQ ID No:268) ; SET 114: (SEQ ID No:269; SEQ
ID No:270) ; SET 115: (SEQ ID No:271; SEQ ID No:272) ; SET 116:
(SEQ ID No:273; SEQ ID No:274) ; SET 117: (SEQ ID No:275; SEQ ID
No:276) ; SET 118: (SEQ ID No:277; SEQ ID No:278) ; SET 119: (SEQ
ID No:279; SEQ ID No:280; SEQ ID No:281) ; SET 120: (SEQ ID
30 No:282; SEQ ID No:283; SEQ ID No:276) ; SET 121: (SEQ ID No:284;
SEQ ID No:285) ; SET 122: (SEQ ID No:286; SEQ ID No:287; SEQ ID
No:288) ; SET 123: (SEQ ID No:289; SEQ ID No:290) ; SET 124: (SEQ
ID No:291; SEQ ID No:292) ; SET 125: (SEQ ID No:293; SEQ ID
No:294; SEQ ID No:295) ; SET 126: (SEQ ID No:296; SEQ ID No:297) ;
35 SET 127: (SEQ ID No:298; SEQ ID No:299; SEQ ID No:300) ; SET 128:
(SEQ ID No:301; SEQ ID No:302; SEQ ID No:288) ; SET 129: (SEQ ID
No:303; SEQ ID No:304) ; SET 130: (SEQ ID No:305; SEQ ID No:306;

SEQ ID No:307) ; SET 131: (SEQ ID No:308; SEQ ID No:309; SEQ ID
No:310) ; SET 132: (SEQ ID No:311; SEQ ID No:312; SEQ ID No:313) ;
SET 133: (SEQ ID No:314; SEQ ID No:315; SEQ ID No:316) ; SET 134:
(SEQ ID No:317; SEQ ID No:318) ; SET 135: (SEQ ID No:319; SEQ ID
5 No:320; SEQ ID No:321) ; SET 136: (SEQ ID No:322; SEQ ID No:323) ;
SET 137: (SEQ ID No:324; SEQ ID No:325) ; SET 138: (SEQ ID No:326;
SEQ ID No:327; SEQ ID No:328) ; SET 139: (SEQ ID No:329; SEQ ID
No:330) ; SET 140: (SEQ ID No:331; SEQ ID No:332; SEQ ID No:333) ;
SET 141: (SEQ ID No:334; SEQ ID No:335; SEQ ID No:336) ; SET 142:
10 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET 143: (SEQ ID
No:339; SEQ ID No:340; SEQ ID No:341) ; SET 144: (SEQ ID No:342;
SEQ ID No:343; SEQ ID No:344) ; SET 145: (SEQ ID No:345; SEQ ID
No:346) ; SET 146: (SEQ ID No:347; SEQ ID No:348; SEQ ID No:349) ;
SET 147: (SEQ ID No:350; SEQ ID No:351) ; SET 148: (SEQ ID No:352;
15 SEQ ID No:353) ; SET 149: (SEQ ID No:354; SEQ ID No:355) ; SET
150: (SEQ ID No:356; SEQ ID No:357) ; SET 151: (SEQ ID No:358; SEQ
ID No:359; SEQ ID No:360) ; SET 152: (SEQ ID No:361; SEQ ID No:31)
; SET 153: (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET
154: (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET 155: (SEQ
20 ID No:368; SEQ ID No:369; SEQ ID No:300) ; SET 156: (SEQ ID
No:370; SEQ ID No:371) ; SET 157: (SEQ ID No:372; SEQ ID No:373;
SEQ ID No:108) ; SET 158: (SEQ ID No:374; SEQ ID No:375; SEQ ID
No:376) ; SET 159: (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ;
SET 160: (SEQ ID No:380; SEQ ID No:381) ; SET 161: (SEQ ID No:382;
25 SEQ ID No:383; SEQ ID No:384) ; SET 162: (SEQ ID No:385; SEQ ID
No:386; SEQ ID No:387) ; SET 163: (SEQ ID No:388; SEQ ID No:389;
SEQ ID No:390) ; SET 164: (SEQ ID No:391; SEQ ID No:392; SEQ ID
No:393) ; SET 165: (SEQ ID No:394; SEQ ID No:395) ; SET 166: (SEQ
ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET 167: (SEQ ID
30 No:399; SEQ ID No:400; SEQ ID No:117) ; SET 168: (SEQ ID No:401) ;
SET 169: (SEQ ID No:402; SEQ ID No:403) ; SET 170: (SEQ ID No:404;
SEQ ID No:405; SEQ ID No:318) ; SET 171: (SEQ ID No:406; SEQ ID
No:407; SEQ ID No:408) ; SET 172: (SEQ ID No:409; SEQ ID No:410;
SEQ ID No:411) ; SET 173: (SEQ ID No:412; SEQ ID No:413) ; SET
35 174: (SEQ ID No:414; SEQ ID No:415; SEQ ID No:416) ; SET 175: (SEQ
ID No:417; SEQ ID No:418; SEQ ID No:419) ; SET 176: (SEQ ID
No:420; SEQ ID No:421; SEQ ID No:422) ; SET 177: (SEQ ID No:423;

SEQ ID No:424; SEQ ID No:425) ; SET 178: (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET 179: (SEQ ID No:429; SEQ ID No:408) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ ID No:431) ; SET 182: (SEQ ID No:432) ; SET 183: (SEQ ID No:433; SEQ ID No:434) ; SET 184: (SEQ ID No:435; SEQ ID No:436) ; SET 185: (SEQ ID No:437) ; SET 186: (SEQ ID No:438; SEQ ID No:439) ; SET 187: (SEQ ID No:440; SEQ ID No:441) ; SET 188: (SEQ ID No:442) ; SET 189: (SEQ ID No:444) ; SET 190: (SEQ ID No:445) ; SET 191 (SEQ ID No:446 ; SEQ ID No:447) ; SET 192: (SEQ ID No:448) ; SET 193: (SEQ ID No:449) ; SET 194: (SEQ ID No:450): SET 195: (SEQ ID No:451) ; SET 196: (SEQ ID No:452) ; SET 197: (SEQ ID No:453) ; SET 198: (SEQ ID No:454) ; SET 199: (SEQ ID No:455) ; SET 200: (SEQ ID No:456) ; SET 201: (SEQ ID No:457) ; SET 202: (SEQ ID No:458) ; SET 203: (SEQ ID No:459) ; SET 204: (SEQ ID No:460) ; SET 205: (SEQ ID No:461) ; SET 206: (SEQ ID No:462) ; SET 207: (SEQ ID No:463) ; SET 208: (SEQ ID No:464) ; SET 209: (SEQ ID No:465) ; SET 210: (SEQ ID No:466) ; SET 211: (SEQ ID No:467) ; SET 212: (SEQ ID No:468)

3. A polynucleotide library according to Claim 2 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

4. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 1: (SEQ ID No:1 ; SEQ ID No:2) ; SET 4: (SEQ ID No:7 ; SEQ ID No:8) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 21: (SEQ ID No:46 ; SEQ ID No:47) ; SET 24: (SEQ ID No:54 ; SEQ ID No:55 ; SEQ ID No:56) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 38: (SEQ ID No:91 ; SEQ ID

No:92 ; SEQ ID No:93) ; SET 48: (SEQ ID No:115 ; SEQ ID No:116 ;
SEQ ID No:117) ; SET 53: (SEQ ID No:126 ; SEQ ID No:127 ; SEQ ID
No:128) ; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140)
; SET 59: (SEQ ID No:141 ; SEQ ID No:142 ; SEQ ID No:143) ; SET
5 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149) ; SET 64: (SEQ
ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET 66: (SEQ ID
No:162 ; SEQ ID No:163) ; SET 69: (SEQ ID No:168 ; SEQ ID No:169;
SEQ ID No:170) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 85:
(SEQ ID No:204; SEQ ID No:205) ; SET 88: (SEQ ID No:210; SEQ ID
10 No:211) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 97: (SEQ ID
No:230; SEQ ID No:231; SEQ ID No:232) ; SET 104: (SEQ ID No:248;
SEQ ID No:249) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID
No:252) ; SET 112: (SEQ ID No:265 ; SEQ ID No:266) ; SET 113: (SEQ
ID No:267 ; SEQ ID No:268) ; SET 115 ; (SEQ ID No:271 ; SEQ ID
15 No:272) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310)
; SET 132: (SEQ ID No:311 ; SEQ ID No:312 ; SEQ ID No:313) ; SET
134: (SEQ ID No:317 ; SEQ ID No:318) ; SET 137: (SEQ ID No:324 ;
SEQ ID No:325) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) ; SET
147: (SEQ ID No:350 ; SEQ ID No:351) ; SET 155: (SEQ ID No:368 ;
20 SEQ ID No:369 ; SEQ ID No:300) ; SET 175: (SEQ ID No:417 ; SEQ ID
No:418 ; SEQ ID No:419) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ
ID No:431) ; SET 182: (SEQ ID No:432) ; SET 185: (SEQ ID No:437) ;
SET 187: (SEQ ID No:440 ; SEQ ID No:441,

wherein said sequences are useful in
25 differentiating a normal cell from a cancer cell.

5. A polynucleotide library according to Claim
4 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

6. A polynucleotide library according to Claim 4
35 wherein the pool of polynucleotide sequences or subsequences

correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78)
; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 131: (SEQ ID
No:308 ; SEQ ID No:309 ; SEQ ID No:310) ; SET 145: (SEQ ID No:345
; SEQ ID No:346) and SET 181: (SEQ ID No:431)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET 38: (SEQ ID No:91 ; SEQ ID No:92 ; SEQ ID No:93)
; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140); SET 61:
(SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149); SET 69: (SEQ ID
No:168 ; SEQ ID No:169 ; SEQ ID No:170) and SET 182: (SEQ ID
No:432).

7 A polynucleotide library according to Claim
6 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
20 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 8. A library according to anyone Claim 1 or 2
wherein the pool of polynucleotide sequences or subsequences
correspond substantially to any combination of at least one
polynucleotide sequence selected among those included in each
one of predefined polynucleotide sequences sets comprising:

30 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 26: (SEQ ID No:59; SEQ ID No:60 ; SEQ ID No:61) ; SET 32:
(SEQ ID No:76; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID
No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ
ID No:99) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;SEQ ID No:137)
; SET 64: (SEQ ID No:156 ; SEQ ID No:157; SEQ ID No:158) ; SET
35 107: (SEQ ID No:255 ; SEQ ID No:256) ; SET 119: (SEQ ID No:279 ;

SEQ ID No:280 ; SEQ ID No:281) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 165: (SEQ ID No:394 ; SEQ ID No:395) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416) and SET 188: (SEQ ID No:442),

wherein said sequences are useful in detecting a hormone sensitive tumor cell

9. A polynucleotide library according to Claim 8 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10. A library according to Claim 8 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346); SET 149: (SEQ ID No:354 ; SEQ ID No:355) and SET 169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99); SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137); SET 119: (SEQ ID

No:279; SEQ ID No:280 ; SEQ ID No:281) and SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416)

11. A polynucleotide library according to Claim 10 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

12. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 8: (SEQ ID No:16) ; SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 25: (SEQ ID No:57 ; SEQ ID No:58) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET 91: (SEQ ID No:216 ; SEQ ID No:217) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327 ; SEQ ID No:328) ; SET 139: (SEQ ID No:329 ; SEQ ID No:330) ; SET 141: (SEQ ID No:334 ; SEQ ID No:335 ; SEQ ID No:336) ; SET 158: (SEQ ID No:374 ; SEQ ID No:375 ; SEQ ID No:376) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 180: (SEQ ID No:430) and SET 186: (SEQ ID No:438 ; SEQ ID No:439),

wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

13. A polynucleotide library according to Claim 12 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

14. A library according to Claim 12 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136; SEQ ID No:137); SET 91: (SEQ ID No:216 ; SEQ ID No:217) and SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23; SEQ ID No:24) ; SET 40: (SEQ ID No:97; SEQ ID No:98 SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) and SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336).

15. A polynucleotide library according to Claim 14 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

16. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or

subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5 SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)
; SET 22: (SEQ ID No:48 ; SEQ ID No:49 ; SEQ ID No:50) ; SET 23:
(SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET 26: (SEQ ID
No:59 ; SEQ ID No:60 ; SEQ ID No:61) ; SET 28: (SEQ ID No:65 ; SEQ
ID No:66 ; SEQ ID No:67) ; SET 31: (SEQ ID No:73 ; SEQ ID No:74 ;
10 SEQ ID No:75) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID
No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 49: (SEQ ID
No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;
SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID
No:158) ; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 77: (SEQ ID
15 No:186) ; SET 81: (SEQ ID No:194 ; SEQ ID No:195) ; SET 95: (SEQ
ID No:226 ; SEQ ID No:227) ; SET 131: (SEQ ID No:308 ; SEQ ID
No:309 ; SEQ ID No:310) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327
; SEQ ID No:328) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ
ID No:333) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162:
20 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET 164: (SEQ ID
No:391 ; SEQ ID No:392 ; SEQ ID No:393) ; SET 165: (SEQ ID No:394
; SEQ ID No:395) and SET 183: (SEQ ID No:433 ; SEQ ID No:434),

 wherein said sequences are useful in
differentiating antracycline-sensitive tumors from
25 antracycline-insensitive tumors.

17. A polynucleotide library according to Claim
16 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
30 least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

18. A library according to Claim 16 wherein the
35 pool of polynucleotide sequences or subsequences correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

5 SET N° 32: (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78)
; SET N°136: (SEQ ID No:322 ; SEQ ID No:323) ; SET N° 145: (SEQ ID
No:345; SEQ ID No:346) ; SET N° 149: SEQ ID No:354; SEQ ID No:355)
; SET N°169: (SEQ ID No:402 ; SEQ ID No:403)

10 and of at least one polynucleotide sequence
selected among those included in each one of predefined
polynucleotide sequences sets comprising:

15 SET No 11: (SEQ ID No:22; SEQ ID No:23 ; SEQ ID
No:24); SET No 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ;
SET No 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET
No 119: (SEQ ID No:279 ; SEQ ID No:280 ; SEQ ID No:281) ; SET No
174: (SEQ ID No:414 ; SEQ ID No:415; SEQ ID No:416).

20 19. A polynucleotide library according to Claim
18 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
predefined sets.

25 20. A library according to anyone of Claims 1 or
2 wherein the pool of polynucleotide sequences or
subsequences correspond substantially to any combination of
at least one polynucleotide sequence selected among those
included in each one of predefined polynucleotide sequences
sets comprising

30 SET No 14 (SEQ ID No:30; SEQ ID No:31) ; SET No 23
(SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET No 25 (SEQ ID
No:57; SEQ ID No:58) ; SET No 27 (SEQ ID No:62; SEQ ID No:63; SEQ
ID No:64) ; SET No 28 (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;
SET No 32 (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET No 39
35 (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET No 41 (SEQ ID

No:100; SEQ ID No:101; SEQ ID No:78) ; SET No 44 (SEQ ID No:106;
SEQ ID No:107; SEQ ID No:108) ; SET No 48 (SEQ ID No:115; SEQ ID
No:116; SEQ ID No:117) ; SET No 51 (SEQ ID No:122; SEQ ID No:78) ;
SET No 64 (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET No
5 81 (SEQ ID No:194; SEQ ID No:195) ; SET No 83 (SEQ ID No:199; SEQ
ID No:200) ; SET No 91 (SEQ ID No:216; SEQ ID No:217) ; SET No 96
(SEQ ID No:228; SEQ ID No:229) ; SET No 99 (SEQ ID No:235; SEQ ID
No:236; SEQ ID No:237) ; SET No 108 (SEQ ID No:257; SEQ ID No:258)
; SET No 110 (SEQ ID No:262; SEQ ID No:200) ; SET No 116 (SEQ ID
10 No:273; SEQ ID No:274) ; SET No 117 (SEQ ID No:275; SEQ ID No:276)
; SET No 118 (SEQ ID No:277; SEQ ID No:278) ; SET No 120 (SEQ ID
No:282; SEQ ID No:283; SEQ ID No:276) ; SET No 126 (SEQ ID No:296;
SEQ ID No:297;) ; SET No 142 (SEQ ID No:337; SEQ ID No:338; SEQ ID
No:117) ; SET No 144 (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344)
15 ; SET No 149 (SEQ ID No:354; SEQ ID No:355) ; SET No 152 (SEQ ID
No:361; SEQ ID No:31) ; SET No 153 (SEQ ID No:362; SEQ ID No:363;
SEQ ID No:364) ; SET No 154 (SEQ ID No:365; SEQ ID No:366; SEQ ID
No:367) ; SET No 157 (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108)
; SET No 159 (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET
20 No 162 (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET No 166
(SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET No 167 (SEQ ID
No:399; SEQ ID No:400; SEQ ID No:117) ; SET No 168 (SEQ ID No:401)
; SET No 171 (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET
No 172 (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET No 173
25 (SEQ ID No:412; SEQ ID No:413) ; SET No 176 (SEQ ID No:420; SEQ ID
No:421; SEQ ID No:422) ; SET No 177 (SEQ ID No:423; SEQ ID No:424;
SEQ ID No:425) ; SET No 178 (SEQ ID No:426; SEQ ID No:427; SEQ ID
No:428) ; SET No 179 (SEQ ID No:429; SEQ ID No:408) ; SET No 184
(SEQ ID No:435; SEQ ID No:436) ; SET No 185 (SEQ ID No:437),

30 wherein said sequences are useful in classifying
good and poor prognosis primary breast tumors.

21. A polynucleotide library according to Claim
20 wherein said polynucleotide sequences or subsequences
35 thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at

least 50%, preferably 75% and more preferably 100% of the predefined sets.

22. A library according to Claim 20 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 23 (SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET N° 25 (SEQ ID No:57 ; SEQ ID No:58) ; SET N° 32 (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET N° 41 (SEQ ID No:100 ; SEQ ID No:101 ; SEQ ID No:78) ; SET N° 48 (SEQ ID No:115 ; SEQ ID No:116 ; SEQ ID No:117) ; SET N° 51 (SEQ ID No:122 ; SEQ ID No:78) ; SET N° 64 (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET N° 81 (SEQ ID No:194 ; SEQ ID No:195) ; SET N° 83 (SEQ ID No:199 ; SEQ ID No:200) ; SET N° 91 (SEQ ID No:216 ; SEQ ID No:217) ; SET N° 99 (SEQ ID No:235 ; SEQ ID No:236 ; SEQ ID No:237) ; SET N° 110 (SEQ ID No:262 ; SEQ ID No:200) ; SET N° 116 (SEQ ID No:273 ; SEQ ID No:274) ; SET N° 142 (SEQ ID No:337 ; SEQ ID No:338 ; SEQ ID No:117) ; SET N° 144 (SEQ ID No:342 ; SEQ ID No:343 ; SEQ ID No:344) ; SET N° 149 (SEQ ID No:354 ; SEQ ID No:355) ; SET N° 162 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET N° 167 (SEQ ID No:399 ; SEQ ID No:400 ; SEQ ID No:117) ; SET N° 171 (SEQ ID No:406 ; SEQ ID No:407 ; SEQ ID No:408) ; SET N° 172 (SEQ ID No:409 ; SEQ ID No:410 ; SEQ ID No:411) ; SET N° 173 (SEQ ID No:412 ; SEQ ID No:413) ; SET N° 176 (SEQ ID No:420 ; SEQ ID No:421 ; SEQ ID No:422) ; SET N° 177 (SEQ ID No:423 ; SEQ ID No:424 ; SEQ ID No:425) ; SET N° 178 (SEQ ID No:426 ; SEQ ID No:427 ; SEQ ID No:428) ; SET N° 179 (SEQ ID No:429 ; SEQ ID No:408) ; SET N° 184 (SEQ ID No:435 ; SEQ ID No:436) ; SET N° 185 (SEQ ID No:437),

and at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 14 (SEQ ID No:30 ; SEQ ID No:31) ; SET No 27 (SEQ ID No:62 ; SEQ ID No:63 ; SEQ ID No:64) ; SET No 28 (SEQ ID

No:65 ; SEQ ID No:66 ; SEQ ID No:67) ; SET No 39 (SEQ ID No:94 ;
SEQ ID No:95 ; SEQ ID No:96) ; SET No 44 (SEQ ID No:106 ; SEQ ID
No:107 ; SEQ ID No:108) ; SET No 96 (SEQ ID No:228 ; SEQ ID
No:229) ; SET No 108 (SEQ ID No:257 ; SEQ ID No:258) ; SET No 117
5 (SEQ ID No:275 ; SEQ ID No:276) ; SET No 118 (SEQ ID No:277 ; SEQ
ID No:278) ; SET No 120 (SEQ ID No:282 ; SEQ ID No:283 ; SEQ ID
No:276) ; SET No 126 (SEQ ID No:296 ; SEQ ID No:297) ; SET No 152
(SEQ ID No:361 ; SEQ ID No:31) ; SET No 153 (SEQ ID No:362 ; SEQ
ID No:363 ; SEQ ID No:364) ; SET No 154 (SEQ ID No:365 ; SEQ ID
10 No:366 ; SEQ ID No:367) ; SET No 157 (SEQ ID No:372 ; SEQ ID
No:373 ; SEQ ID No:108) ; SET No 159 (SEQ ID No:377 ; SEQ ID
No:378 ; SEQ ID No:379) ; SET No 166 (SEQ ID No:396 ; SEQ ID
No:397 ; SEQ ID No:398) ; SET No 168 (SEQ ID No:401),

wherein the combination of overexpression of the
15 genes identified by said first group of cluster sequences
with the underexpression of the genes identified by said
second group of cluster sequences are useful in classifying
good and poor prognosis primary breast tumors.

20 23. A polynucleotide library according to Claim
22 wherein said polynucleotide sequences or subsequences
thereof of said pool correspond to any combination of at
least one polynucleotide selected among those included in at
least 50%, preferably 75% and more preferably 100% of the
25 predefined sets.

24. A polynucleotide library according to anyone
of Claims 1 to 23 wherein said tumor cells are breast tumor
cells.

30 25. A polynucleotide library according to any of
Claims 1 to 23 wherein said polynucleotides are immobilized
on a solid support in order to form a polynucleotide array.

26. A polynucleotide library according to Claim 25 wherein the support is selected from the group comprising a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

5

27. A polynucleotide array useful for prognosis or diagnostic of tumor comprising an immobilized polynucleotide library according to Claims 1 to 3.

10

28. A polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of immobilized polynucleotide sequences sets according to claims 4 to 7.

15

29. A polynucleotide array useful to detect a hormone sensitive tumor cell comprising any combination of immobilized polynucleotide sequences sets according to claims 8 to 11.

20

30. A polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of immobilized polynucleotide sequences sets according to claims 12 to 15.

25

31. A polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of immobilized polynucleotide sequences sets according to claims 16 to 19.

30

32. A polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any

combination of immobilized polynucleotide sequences sets according to claim 20 to 23.

5 33. A method of detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient and

10 b) reacting said polynucleotide sample obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any combination of the polynucleotide sequences of the polynucleotide library of Claims 1 to 23 or any combination of expression products encoded by any of the polynucleotide sequences of the
15 libraries of Claims 1 to 23 and

c) detecting the reaction product of step (b).

20 34. A method for detecting differentially expressed polynucleotide sequences according to Claim 33 wherein said polynucleotide sample is labeled before its reaction step.

25 35. A method for detecting differentially expressed polynucleotide sequences according to Claim 34 wherein the label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent labels.

30 36. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 35 further comprising obtaining a control polynucleotide sample, reacting said control sample with said probe

detecting a control sample reaction product and comparing the amount of said polynucleotide sample reaction product to the amount of said control sample reaction product.

5 37. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 36 wherein the polynucleotide sample is cDNA, RNA or mRNA.

10 38. A method for detecting differentially expressed polynucleotide sequences according to Claim 37 wherein mRNA is isolated from said polynucleotide sample and cDNA is obtained by reverse transcription of said mRNA.

15 39. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 38 wherein said reaction step is performed by hybridising the polynucleotide sample with the probe.

20 40. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 39 wherein said method is used for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with cancer.

25 41. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 40 wherein the cancer is breast cancer.

30 42. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 41 wherein the product encoded by any of the polynucleotide sequences or polynucleotide sequences sets is involved in a receptor-ligand reaction on which detection is based.

43. A method for screening an anti-tumor agent comprising the method of Claim 33 wherein said polynucleotide sample is obtained from a patient treated with the anti-tumor agent to be screened.

Figure 1

Normal Breast

Figure 1A

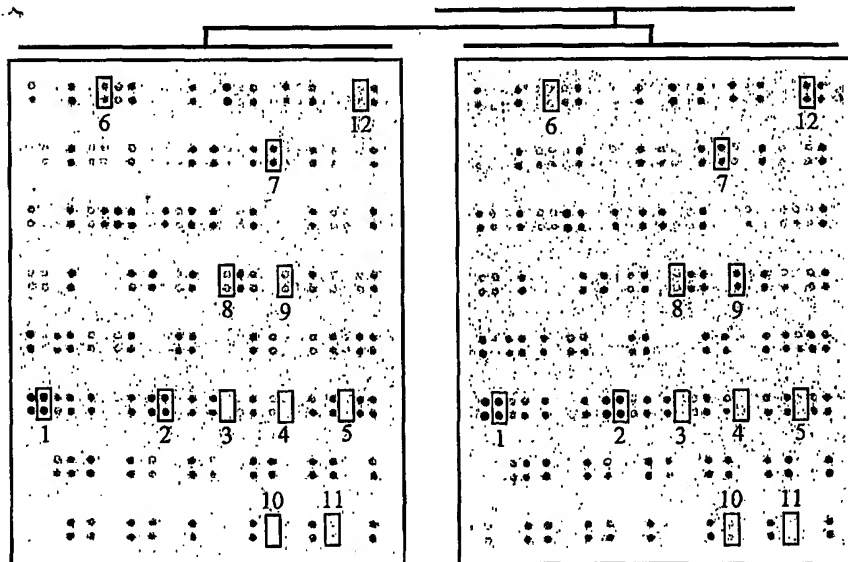
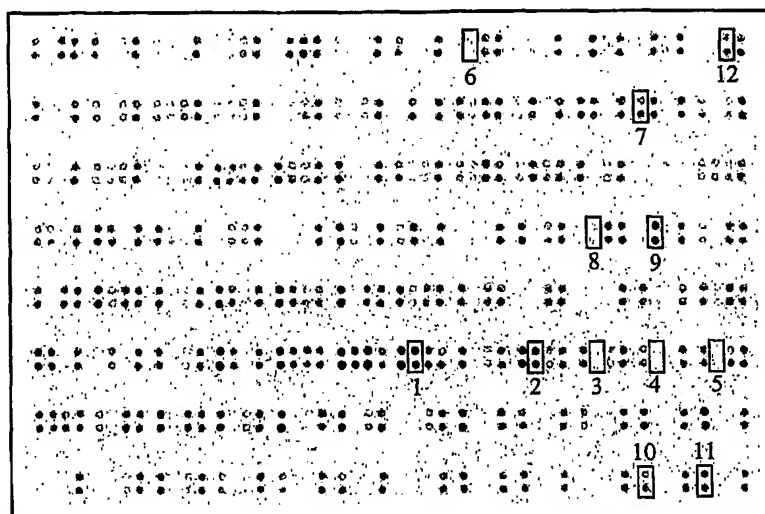


Figure 1B

ER-

ER+

Figure 1C

Breast cancer

Figure 2

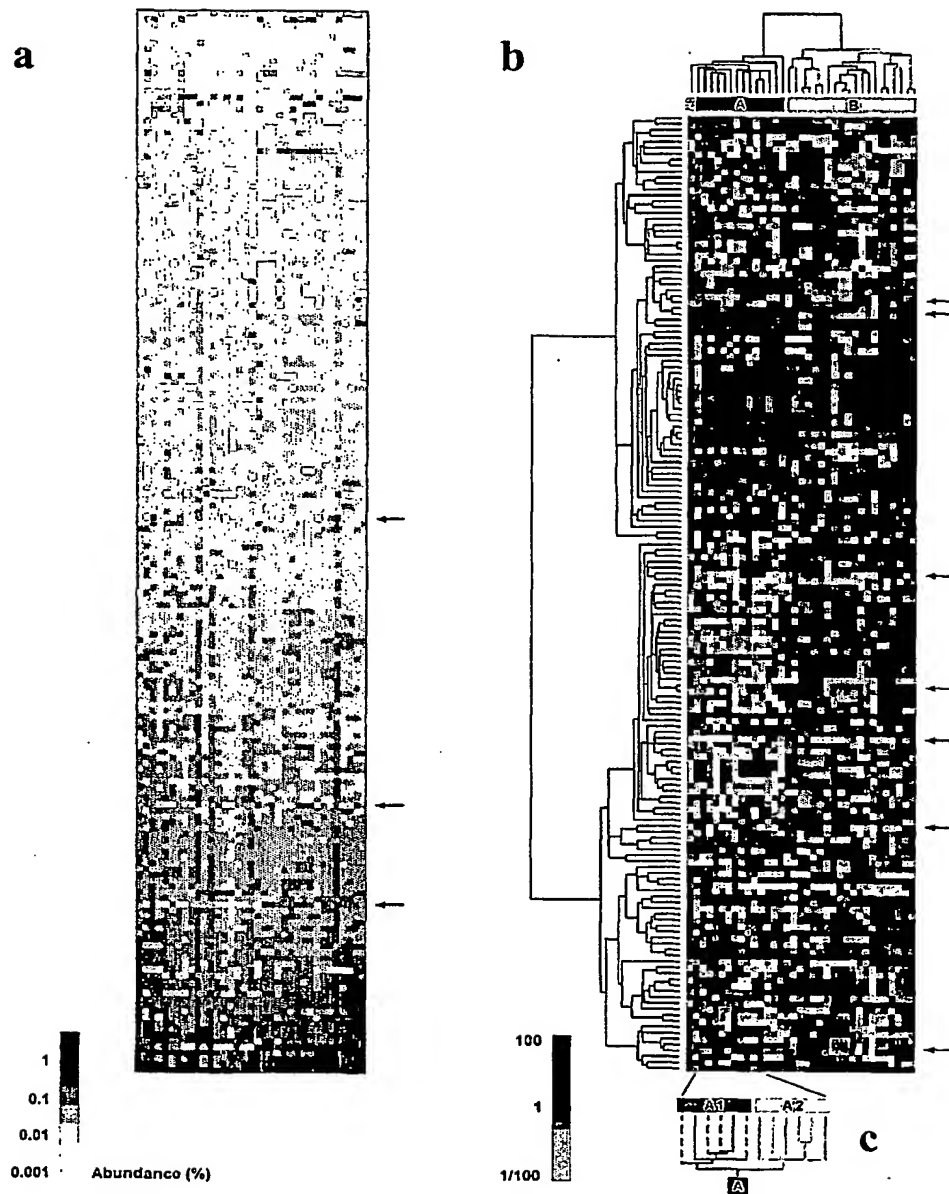


Figure 3

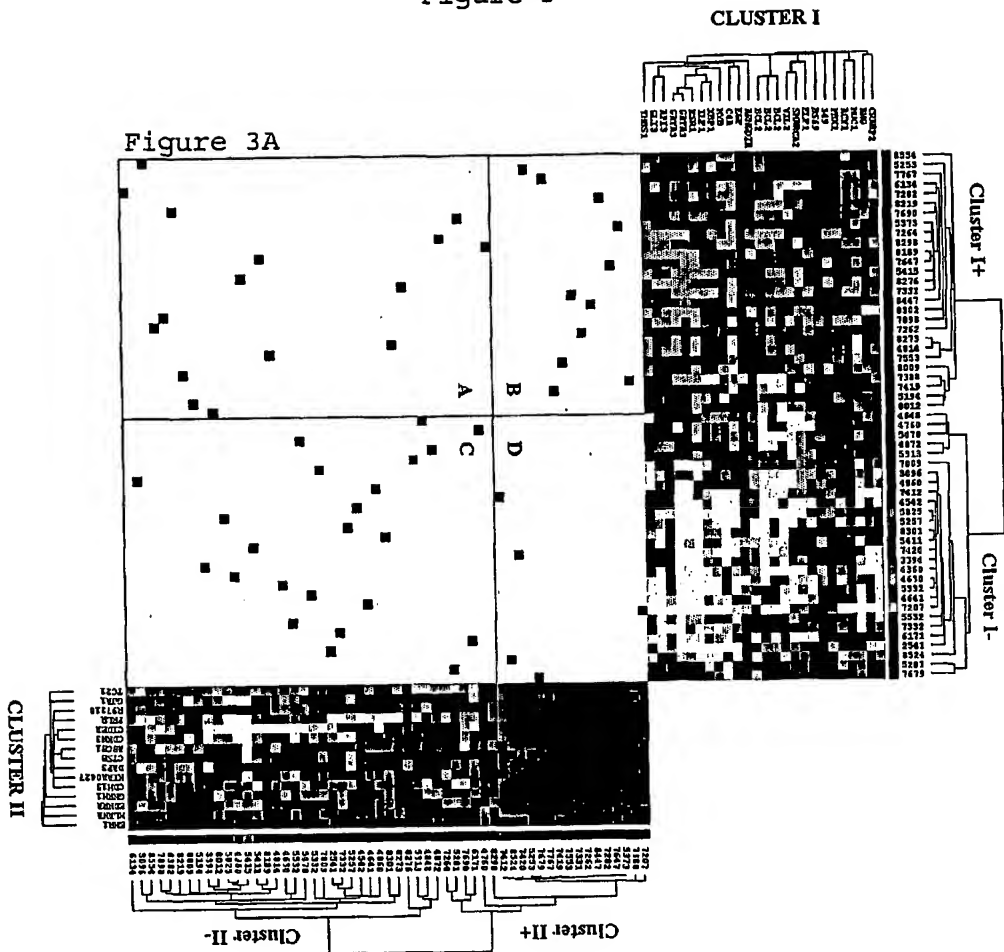


Figure 3C

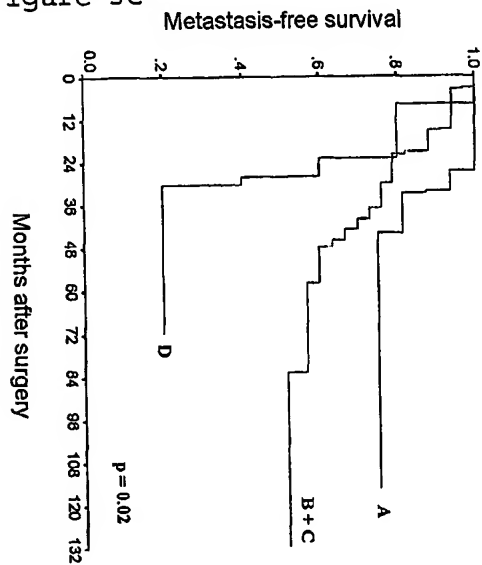


Figure 3B

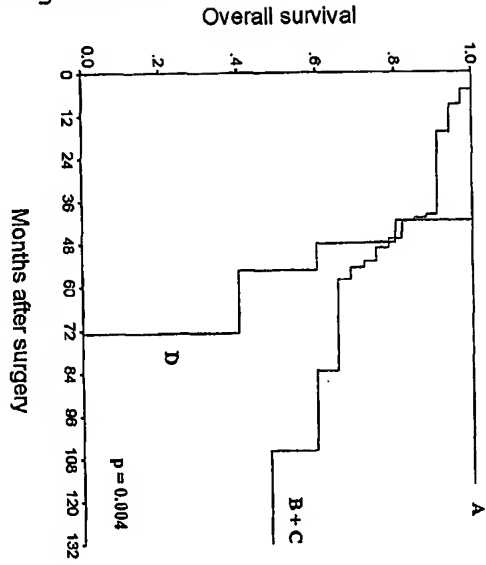


Figure 4

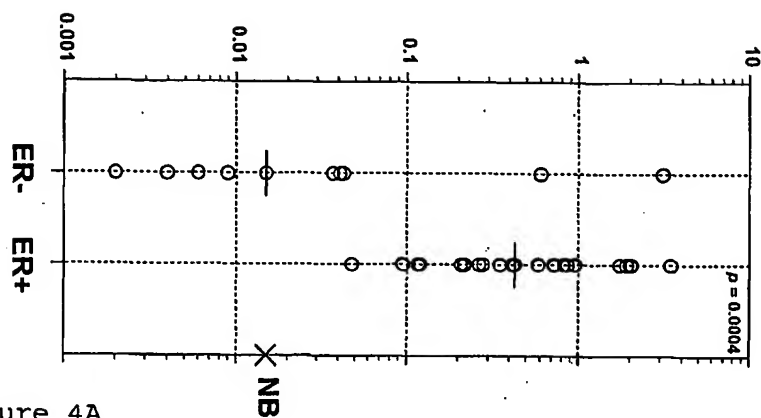


Figure 4A

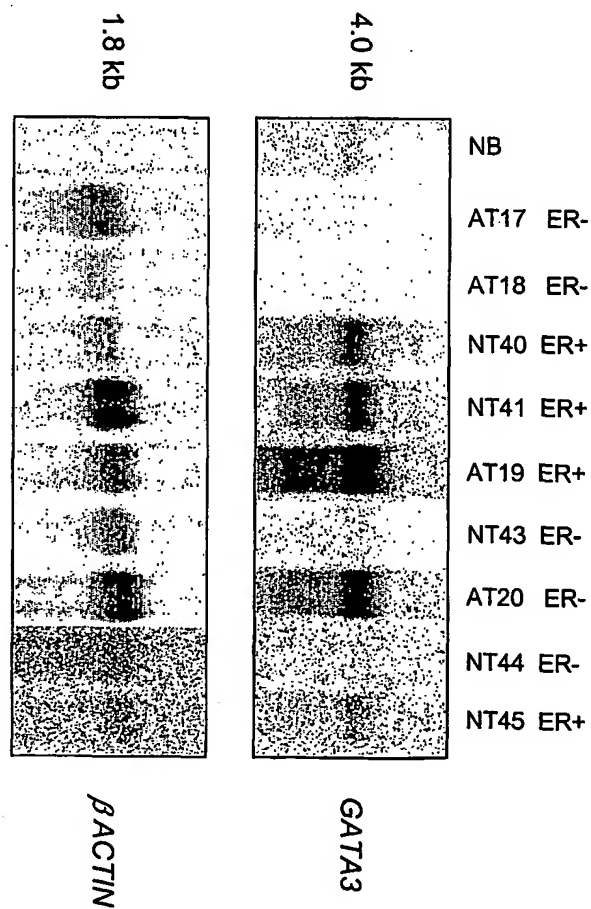


Figure 4B

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<110> François Bertucci
Rémi Houlgatte
Daniel Birnbaum
Catherine Nguyen
Patrice Viens
Fert, vincent

<120> cDNA arrays and their use for gene expression profiling.

<130> 10813PCT-December-2001-ipsogen

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gtttggaaca tagcgaatcc gaatggatct gatgaaacct gtaccaggtg cttttatttt 2520
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gtggacttga aaatacacag tggg ctagtc cagtgtctat atttaaactt gttcttttct 2820
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caaagaatga ggttagaaga ctgcagcttg gagtctct ct aggttttcaa ctattttctc 3240
acaatttgaa cacttgacgg ttgtcccttt taattttatt gaagtgtat ttttttaaat 3300
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```

<210> 7

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(300)

<223> 3' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 7

```

tncaagagac aggggttnngc acattgccca ggatggtctc aaactcctag agttgagcta 60
tccacccacc tttggcctnc caaagtgtcg ggatcacagg cgtgagtcac tgnntccagc 120
accatcttgg aggtcttcta aagcccaggc cccacgccga gcttctgagt caataaagaa 180
gtctgcattt ctaacaagct tctaggggat gctgctgctg ctgctggtcc aggggccccca 240
ctttgaagaa ccactgcact gggtntttcc tctgggaccc gaatgcctgt gcttctcccc 300

```

<210> 8

<211> 369

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(369)
<223> 5' terminal sequence. ests, weakly similar
to alu7_human alu subfamily sq sequence
contamination warning entry [h.sapiens] (EST
T81919) gene.

<400> 8
cctaacgcag gtttccccgc aaatgactgg tcacgcggga ctgaacaccg cacaggcagg 60
aggcatggca agggtaagtg aa ctgaagca ctttcaatac ttcctaccta accgcgggct 120
ttccctccga gtaatgcgta aaatgggacc acgtggccca ctctgtttt tctctttggg 180
ctctccacgt gccactcatg cttggaagag acagatttct ttctaggata aagatctctg 240
ccccatttct gtcttttaaa atggagaatt ctttaaagaa gtagggacag cttncagggt 300
cagggcagtt tgggaaagtn acaggggcct aattgtgttc cgtggaaacn ggggtaggag 360
gtttgcttt 369

<210> 9
<211> 255
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(255)
<223> 3' terminal sequence. cyclin d1 (prad1:
parathyroid adenomatosis 1) (CCND1) gene.

<400> 9
aaagacagtt tttgggtaat cttttncttt tgcttaagtc agagatggaa gggggaaaga 60
gcaaaggaaa aaacaaccaa caacaaggag aatgaagctt tcccttcttg tatcaaaatg 120
ctccggagag gagggactnt cagtggagca cctggggccg gctccgcctc gctgcgggtg 180
gcggtggcgc cctngcctg gcgccttcag atgtccacgt cccgcacgtc ggtgggtntg 240
caagccaggt ccacc 255

<210> 10
<211> 1325
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1325)
<223> cyclin d1 (prad1: parathyroid adenomatosis
1) (CCND1) gene.

<400> 10

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```
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gcgcgggggca gcagaagcga gagccgagcg cggacccagc caggaccac agccctcccc 120
agctgcccag gaagagcccc agccatggaa caccagctcc tgtgctgcga agtggaaacc 180
atccgcgcg cgtaccccga tgccaacctc ctcaacgacc ggggtgctgcg ggccatgctg 240
aaggcggagg agacctgcgc gccctcgggtg tcctacttca aatgtgtgca gaaggaggtc 300
ctgccgtcca tgcggaagat cgtcgccacc tggatgctgg aggtctgcga ggaacagaag 360
tgcgaggagg aggtcttccc gctggccatg aactacctgg accgcttct gtcgctggag 420
cccgtgaaaa agagccgcct gcagctgctg ggggccactt gcatgttcgt ggcctctaag 480
atgaaggaga ccatccccct gacggccgag aagctgtgca tctacaccga cggctccatc 540
cggcccgagg agctgctgca aatggagctg ctcttggtga acaagctcaa gtggaacctg 600
gccgcaatga cccgcacga ttctattgaa cacttcctct ccaaaatgcc agaggcggag 660
gagaacaaac agatcatocg caaacacg cg cagaccttcg ttgcctcttg tgccacagat 720
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cggcccccag tgctccacat gacagtcctt cctctccgga gcattt tgat accagaaggg 1140
aaagcttcat tctccttgtt gttggttgtt ttttctttg ctctttcccc cttccatctc 1200
tgacttaagc aaaagaaaaa gattacccaa aaactgtctt taaaagagag agagagaaaa 1260
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaa 1325
```

<210> 11

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. signal transducer and
activator of transcription 1, 91kd (STAT1) gene.

<400> 11

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ttaggaagtt caacattttg ggcacgcaca caaaagtgat gaacatggag gagtccacca 120
atggcagctc ggcggtgaa tttcggcacc tgcaattgaa agaacaga aa aatgctggca 180
ccagaacgaa tgagggtcct ctcatcgta ctgaagagct tcaactccctt agttttgaaa 240
cccaattgtg ccagcctggg tttggttaatt gacctcgaga cgacctctct gcccgttgtg 300
ggtgatctcc aacgtcagcc agtcccgag cggttggggc ctccattcct ttgggtacaa 360
catgctgggt nggcgggaac ccgggg antc tgttcttnt ttcctggact ccaccatgtg 420
ncacgggtggg gtttcagntt ttcagaagt 449
```

<210> 12

<211> 4003

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4003)

<223> signal transducer and activator of
transcription 1, 91kd (STAT1) gene.

<400> 12

```
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gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctgcacagtc 120
ttggcaccta acgtgctgtg cgtagctgct cctttggttg aatccccagg ccttgtgttg 180
ggcacaaagt gcagagatgt ctgagtggtg cgaacttcag cagcttgact caaaattcct 240
ggagcaggtt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc 300
acagtgggta gaaaagcaag actgggagca cgctgccaat gatgttt cat ttgccaccat 360
ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttggagaa 420
taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca 480
ggaagaccca atccagatgt ctatgatcat ttacagctgt ctgaaggaa aaaggaaaat 540
tctggaaaaa ccccagagat ttaat caggc tcagtcgggg aatattcaga gcacagtgt 600
gttagacaaa cagaaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg 660
tatagagcat gaaatcaaga gcctggaaga tttacaagat gaatatgact tcaaatgcaa 720
aaccttgacg aacagagaac acgagaccaa tgggtgtggc aagagtgtac agaaacaaga 780
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gctttggaat gaaagcatcc tagaactcat taaaaaacac ctgctccctc tctggaatga 1920
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gccggggacc ttctgtctgc ggttcagtga gagctcccgg gaaggggcca tcacattcac 2040
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gtagataaac tcagaaattt aattcatgtt tcttaaatgg gctactttgt cctttttgtt 3360
attaggggtg tatttagtct att agccaca aaattgggaa aggagtagaa aaagcagtaa 3420
```

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ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt 3480
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gcgaatgggt ccattctctc tcctgtactt tttccagaca cttttttgag tggatgatgt 36 00
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tctcagtttt tatatagatg gcgagaacct aagtttcagt tgattttaca attgaaatga 3960
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<210> 13

<211> 167

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(167)

<223> 3' terminal sequence. fibroblast growth

factor receptor 2 (bacteria -expressed kinase,
keratinocyte growth factor receptor, craniofacial
dysostosis 1, crouzon syndrome, pfeiffer syndrome,
jackson-weiss syndrome) (FGFR2) gene.

<400> 13

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ccacctctgc tcggtgaaaa ttaagaaatt atgtgtaaga acagcattta gcaaatagct 60
attaaaaaaa gagagaccaa ttttctag gt gcattgggac atccatttaa antcaatata 120
aaaaataact ccttgtaaatt ntataatata ttattttatac ntaattt 167

```

<210> 14

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. fibroblast growth

factor receptor 2 (bacteria -expressed kinase,
keratinocyte growth factor receptor, craniofacial
dysostosis 1, crouzon syndrome, pfeiffer syndrome,
jackson-weiss syndrome) (FGFR2) gene.

<400> 14

```

ggacacagaa tggataagcc agccaactgc accaacgaac tgtacatgat gatgaggagc 60
tgttggcatg cagtgcctcc cagagaccaa cgttcaagca gttggtagaa gacttggatc 120
gaattctcac tctcacaacc aatgaggaaat acttggacct cagccaacct ctogaacagt 180
attcacctag ttaccctgac ac aagaagtt cttgttcttc aggagatgat tctgtttttt 240
ctccagaccc catgccttac gaaccatgcc ttctcagta tccacacata aacgggcagt 300
gttttaaaac atgaatgact gtgtctggcc tgncccaa acagggacag gcaactggggg 360
aacctaggct acattnaggc aggggaggac cttgccttc ccaggngttt gttt 414

```

<210> 15
<211> 4667
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4667)
<223> fibroblast growth factor receptor 2
(bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson -weiss syndrome) (FGFR2) gene.

<400> 15
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gcgtacctgg cccggcgcgg cgactgctct c cgggctggc gggggccggc cgcgagcccc 120
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cccaccgcag gctgaaggca ttgcgcgtag tccatgccc tagaggaagt g tgcagatg 540
gattaacgtc cacatggaga tatggaagag gaccggggat tggtagcgta accatggtca 600
gctggggctg tttcatctgc ctggtcgtg tcaccatggc aaccttgtcc ctggcccggc 660
cctccttcag tttagttag gataccacat tagagccaga agagccacca accaaatacc 720
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ggaaaaatac ttttgccttc agggaaaatg gtataacgtt aatttattaa taaattggta 3780
atatacaaaa caattaatca tttatagttt tttttgta ttaagtggca tttctatgca 3840
ggcagcacag cagactagtt aatctattgc ttggacttaa ctagttatca gatcctttga 3900
aaagagaata tttacaatat atgactaatt tggggaaaat gaagttttga tttattttgtg 3960
tttaaatgct gctgtcagac gattgttctt agacctct a aatgccccat attaaaagaa 4020
ctcattcata ggaagggtgt tcatcttggt gtgcaaccct gtcattacgt caacgcaacg 4080
tctaactgga ctcccaaga taaatggtac cagcgtcctc ttaaaagatg ccttaatcca 4140
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ccttctgctt ctgagttgca cattaatcag attagcctga ttctcttcag tgaattttga 4260
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cagacaaaat atcgccgttg ttcttctgt actaaagtat tgtgttttgc tttggaaca 4500
cccactcact ttgcaatagc cgtgcaagat gaatgcagat tacactgatc ttatgtgtta 4560
caaaattgga gaaagtattt aataaaacct gtttaatttt atactgacaa taaaaatgtt 4620
totacagata ttaatgttaa caagaca aaa taaatgtcac gcaactt 4667

```

<210> 16

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 3' terminal sequence. ests (EST T89980)
gene.

<400> 16

```

gtgttgagct cccaaaaggc ttaaaacttg ctttgtgaat gaatgatctt aaatcactag 60
tgaagatgat catggggcat ttgcacatta aagaactaaa atgaaatgaa aaagccatga 120
ctcctcactt aatgctatta aaaaaaaatc tgatttggtg aattaacccc acttctcata 180
gtttaatttg gtaatcaacg ttcttgggaa ttc aggttct catgggcacc ctaatagtgt 240
ttagggccgg ggttctgag gctgctgggg gtgatccga ggaacaagaa gctgccctat 300
taaaagtaat ctacttgagt ttttcccgag tcttggggag ttgttcccta ctgtggggct 360
acttataggg gtagggcccc ccaaatccct cacacttagg tcggccctgc tggcttgctg 420
tggggctctg aaangcagcc gctaggangt cccaagcct naacttacc attttctggc 480

```

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ctg

483

<210> 17
<211> 400
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(400)
<223> 3' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 17
ntttatatat attgaacata aattaaaaga atttataaaa cagccacctt tttacagaat 60
aaatgcagac tgaattataa atgcacctcc acgttgaagt tgttttgagt tgcttttcat 120
tttccaataa taaataaata gaatttgttc ttgagtttta gatccacctg agccacggca 180
ggactctaag tcatgaatgg gctttcttcc ctgggtcgct cctgtgcgca gatgntgagt 240
gtgctgaggt tacagatttc attggcccac cagcgtgtat gc tacccttt cgggggtggg 300
cattcgctca ttaattcggg cccagncctt cgcgctttct ttcaaaactc cgggatcttg 360
tgcntggagg cgaggnaccc ctctgatggg cttcccgagg 400

<210> 18
<211> 490
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(490)
<223> 5' terminal sequence. protein phosphatase 3
(formerly 2b), catalytic subunit, gamma isoform
(calcineurin a gamma) (PPP3CC) gene.

<400> 18
cttggagcac tatacccaca aactgtccg aggggtgctct tatttctaca gttaccctgc 60
agtttgtgaa tttttgcaga acaataattt actatcaatt atcagagccc atgaagccca 120
agatgctggg tatcgaatgt acaggaagag ccaagccaca ggttttccat cacttattac 180
aattttctct gccccaatt acctagatgt ctataacaat aaagctgctg tgttgaaata 240
tgaaaacaat gtcataaata tcaggcagtt taactgttct ccacaccctt actgggcttc 300
caaactttat gggatgtttt cacatgggtc ttgacctttt gttgggggga ccccgacac 360
agaggatggc tgggtaaatg tggntcaaca ttatggntct ggatggacgg aactgatttt 420
ctggatggat ggaagcngga tgggaaggca cttacngttt cgtaaggng g ttcttcggg 480
gnntaggttc 490

<210> 19
<211> 2134
<212> DNA/RNA
<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2134)

<223> protein phosphatase 3 (formerly 2b),
catalytic subunit, gamma isoform (calcineurin a
gamma) (PPP3CC) gene.

<400> 19

```
gggccaccct tagcagcgggt cgcggtcgggt gccgaagcgg tgttccccgc cttagccgct 60
gcgcctccca agagagcggc cgtggggccc tcgtcctgtc agtggcgctc gaggc cggcc 120
tgcggtggcc gcgcccttct ggtgctcgga caccgctgag gagccggggc cgggcacggc 180
tggctgacgg ctccgggcag ctaaggctgc ccgaggagaa ggccggcggc gcggcgtagg 240
cgcacgtccg gcgggctcct ggagcctgga ggagccgag gggacatgt ccgggaggcg 300
cttcacctc tccaccaccg accgcgtcat caa agctgtc ccccttcctc caacccaacg 360
gottactttc aaggaagtat ttgagaatgg gaaacctaaa gttgatgttt taaaaaacca 420
tttggtaaag gaaggacgac tggaagagga agtagcctta aagataatca atgatggggc 480
tgccatcctg aggcaagaga agactatgat agaagtagat gctccaatca cagtatgtgg 540
tgatattcat ggacaattct ttgacctaat gaagttattt gaagttggag gatcacctag 600
taacacacgc tacctctttc tgggtgacta tgtggacaga ggctatttca gtatagagtg 660
tgtgctgtat ttatggagtt taaagattaa tcatoccaaa acattgtttc tgcttcgggg 720
aaatcatgaa tgcaggcatc ttacagacta tttcaccttc aaacaggaat gtc gaatcaa 780
atattcggaa caggtgtatg atgcctgtat ggagacattt gactgtcttc ctcttgctgc 840
cctcttaaac cagcagtttc tctgtgtaca tggaggaatg tcacctgaaa ttactctttt 900
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gcagaacaat aatttactat caattatcag agcccatgaa gcccaagatg ctgggtatcg 1140
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caattaccta gatgtctata acaataaagc tgctgtgttg aaatatgaaa acaatgtcat 1260
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caacatagc tctgatgacg aactgatttc tgatgatgaa gcaga aggaa gcactacagt 1440
tcgtaaggag atcatcagga ataagatcag agccattggg aagatggcac gggctctttc 1500
aattcttcgg caagaaagtg agagtgtgct gactctcaag ggctgactc ccacaggcac 1560
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gcgaatgcc accccgaaag atagcatata ccctgggtgg ccaatgaaat ctgtaacctc 1740
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agtccgtccg tgcacagtg gatctaaaac tcaagaacaa attctattta tttattatt g 1860
gaaaatgaaa agcaactcaa aacaacttca acctggaggt gcatttataa ttcagtctgc 1920
atttattctg taaaaagggt actgttttat aaattctttt aatttatgtt caatatatat 1980
aaaaagtga tctgttttgt ttttcccttt tttctccata attttaagaa atgaatctga 2040
ttgttgtcaa cacatttgtg aagtcttgtg cta taaaggg gaacttcccc taataaaagg 2100
gccttgga a cctcaaacct gggtttctga cccc 2134
```

<210> 20

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. ests (EST T90726)
gene.

<400> 20
atccatttat tatatccaat gctaaacact accacttgga ctctaagata tgtttatgcc 60
tctctgttta ttctagtttt ttaaaaatca aatatacaag atctacaatt atttatatcc 120
aagatgtcta caccactgcc taagaagcta ttaaaatat t tgtatttggtg caatgggnacc 180
cattattcac atgggcctag gattaaaaag tcaatttata ttngngaataa atttntccaa 240
aaaaacca 248

<210> 21
<211> 427
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(427)
<223> 5' terminal sequence. ests (EST T90726)
gene.

<400> 21
taagatacga acgagaaacc tgatttattg ctcaccttc ccttgccctcc ctaatggcaa 60
gcaaaactct gaacatctga aaaggatgta gttctggaca aatcct gact acccagagga 120
aactcactgt gagattgctg ttgatttgaa ggggtgcttc actaaggta tattttaaag 180
tagaataaca catgctgagt gtaaaactggg ctttgattg gtcagctgca gtagtacaaa 240
aacagcatag aatttgagga aaactaaaac tgctatgaga taggctatga ggaaaactta 300
aaactggcta tgtggttagga aatg atgtta aanttatgtg gggaaagttt ttcccctccn 360
tattacttca cattacaggc ctttngaggg gcntctgggc tctgnaccn gtttgatggg 420
cctttga 427

<210> 22
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(294)
<223> 3' terminal sequence. sry (sex determining
region y)-box 4 (SOX4) gene.

<400> 22
tttcttggtt ttcttttttt ttttccgaaa ccaactgccc tccaactgact gcccctgtac 60
cacatcaaac agtctcctct cctccacgcc tccgggggtct ggaagtctc acctcactga 120
tttcacgtag aaaagaaggc ggaggccagc agccgcgcgc ncaagctccc caacgtgcaa 180
atccatttca gtttgaccgt gaacccctt ccagttcgtg tcctcctccg cccccgcccc 240
tagtccccgc tgctggnntc caacggggtt ntccgggtcat ttctagcgc cgg 294

<210> 23
<211> 362
<212> DNA
<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(362)

<223> 5' terminal sequence. sry (sex determining region y)-box 4 (SOX4) gene.

<400> 23

```
ttccggactt gtctgcaccc ccagcaagaa ggcgagttag ttttctagag acttgaagga 60
gtctccccct tcctgcatca ccaccttgggt ttgttttat ttgtcttctt ggtcaagaaa 120
ggaggggaga acccagcgca cccctcccc ctttttttaa acgctgatg aagacagaag 180
gtcccggggt gacgaatttg gccgatggag nat gttttgg gggaacgccg ggactgagag 240
actccacggc agggcgaatt cccgtttggg gctttttttt tcctccctct tttccctt 300
gcccttttg canccgngg agggagntgt tnaagggag ggagggccag ccagtgttga 360
cc 362
```

<210> 24

<211> 2797

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2797)

<223> sry (sex determining region y) -box 4 (SOX4) gene.

<400> 24

```
ttccccagca ttcgagaaac tcctctctac tttagcacgg tctccagact cagccgagag 60
acagcaaaact gcagcgcggt gagagagcga gagagaggga gagagagact ctccagcctg 120
ggaactataa ctctctctcg agaggcggag aactccttcc ccaaattctt tggggacttt 180
tctctcttta cccacctccg cccctgcgag gaggttgagg gccagttcgg ccgcccgcgg 240
cgtcttcccg ttccggcgtgt gcttgcccg gggaaccggg agggcccggc gatcgcgcgg 300
cggccgcggc gagggtgtga gcgcgcgtgg gcgccgcggc agccgaggcc atggtgcagc 360
aaaccaacaa tgccgagaac acggaagcgc tgctggcgg cgagagctcg gactcgggcg 420
ccggcctcga gctgggaate gcctcctccc caacgcccg ctccaccgcc t ccacggggc 480
gcaaggccga cgaccggagc tgggtcaaga ccccgagtgg gcacatcaag cgacctatga 540
acgccttcat ggtgtggtcg cagatcgagc ggcgcaagat catggagcag tcgcccgaca 600
tgcacaacgc cgagatctcc aagcggctgg gcaaacgctg gaagctgctc aaagacagcg 660
acaagatccc ttctattcga gaggcggagc ggctgcgcct caagcacatg gctgactacc 720
ccgactacaa gtaccggccc aggaagaagg tgaagtccgg caacgccaac tccagtcct 780
cggccgcggc ctctccaag ccgggggaga agggagacaa ggtcgggtggc agtggcgggg 840
gcggccatgg gggcggcggc ggccgcgga gcagcaacgc ggggggagga ggcggcggg 900
cgagtggcgg cggcgccaac tccaaaccgg cgagaaaaa gagctgcggc tccaaagtgg 960
cgggcggcgc gggcggtggg gttagcaaac cgcacgcaa gctcatcctg gcaggcggcg 1020
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ccgcgcctt gctgcccctg ggccgcggc ccgaccacca ctgcgtgt ac aaggcgcgga 1140
ctcccagcgc ctccgctcc gcctcctcgg cagcctcggc ctccgcagcg ctccgcggcc 1200
cgggcaagca cctggcggag aagaaggtga agcgcgtcta cctgttcggc ggcctgggca 1260
cgtcgtcgtc gccgtggcg ggcgtggcg cccagcgac cccctggggc 1320
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gcgcgcctc gtccccgcc gccggccgt cgcgcggc caaccgcggc tacgccagcc 1440
tgccgcgcgc ctcccgcc ccgtccagcg cgcctcgca cgcgtcctc tcggcctcgt 1500
cccactcctc ctcttctccc tcctcgggct cctcgtcctc cgacgacgag ttcgaagacg 1 560
acctgctcga cctgaacccc agctcaaaact ttgagagcat gtccctgggc agcttcagtt 1620
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```

cgctcgctcggc gctcgaccgg gacctggatt ttaacttcga gcccggtccc ggctcgact 1680
tcgagttccc ggactactgc acgcccagg tgagcgagat gatctcgga gactggctcg 1740
agtccagcat ctccaacctg gttttcacct actgaa gggc gcgcaggcag ggagaagggc 1800
cggggggggg aggagaggag aaaaaaaaag tgaaaaaag aaacgaaaag gacagacgaa 1860
gagtttaaaag agaaaaggga aaaaagaaag aaaaagtaag cagggtcgt tcgcccgcgt 1920
tctcgtcgtc ggatcaagga gcgcggcggc gttttggacc cgcgtccca tccccacct 1980
tcccgggccg gggaccact ctgcccagcc ggaggagcgc ggaggaggaa gagggtagac 2040
aggggagacc tgtgatgtt gttattgatg ttgtgttgga tggcaaaaa aaaaagcgac 2100
ttcgagtttg ctcccctttg cttgaagaga cccctcccc cttccaacga gcttcggac 2160
ttgtctgcac cccagcaag aaggcgagtt agttttctag agacttgaag gagtctccc 2220
cttctgcat caccaccttg gttttgttt atttgtctt ttggtcaaga aaggagggga 2280
gaacccagcg caccctccc ccccttttt taaacgcgtg atgaagacag aaggctccg 2340
ggtgacgaat ttggccgatg gcagatgtt tgggggaacg ccgggactga gagactccac 2400
gcaggcgaat tccggtttg ggcc ttttt tcttccctct tttcccttg cccctctgc 2460
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cgaactgga gggggttcac ggtcaaaactg aaatggattt gcacgttgg gagctggcg 264 0
cggcggtgc tgggcctcg cttcttttc tacgtgaaat cagtgggtg agacttcca 2700
gaccccgag gcgtggagga gagagactg tttgatgtg tacaggggca gtcagtggag 2760
ggcgagtgtt ttcgaaaaa aaaaagaaa aaaagg 2797

```

<210> 25

<211> 352

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(352)

<223> 5' terminal sequence. ring finger protein 5 (RNF5) gene.

<400> 25

```

acggggggcc caacnanant cgcgagcngg gcgtggcggg cgcgaccttc gaatgt anta 60
tatgtttgga gactgctcgg gaagctgttg tcagtgtgtg tggccacctg tactgttggc 120
catgtcttca tcagtggctg gagacaaggc cagaacggca agagtgtcca gtatgtaaag 180
ctgggatcag cagagagaag gttgtcccg tttatggcg agggagccag aagccccagg 240
atcccagatt aaaaactcca cccgccccc aggcc agaga ccagctccg agagcagagg 300
gggattccag ccatttggtg ataccggggg cttccacttn ttcatttgggt gt 352

```

<210> 26

<211> 543

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(543)

<223> ring finger protein 5 (RNF5) gene.

<400> 26

```

atggcagcag cggaggagga ggacgggggc cccgaaggc caaatcgca gcggggcg 60
gcgggcgca ccttogaatg taatatatgt ttggagactg ctcgggaagc tgtgtcagt 120

```

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```

gtgtgtggcc acctgtactg ttggccatgt cttcatcagt ggctggagac acggc cagaa 180
cggcaagagt gtccagtatg taaagctggg atcagcagag agaaggttgt cccgctttat 240
gggcgaggga gccagaagcc ccaggatccc agattaaaaa ctccaccccg cccccagggc 300
cagagaccag ctccggagag cagaggggga ttccagccat ttggtgatac cgggggcttc 360
cactttcat ttggtgttgg tgcttttccc ttt ggctttt tcaccaccgt ctccaatgcc 420
catgagcctt tccgcccggg tacaggtgtg gatctgggac agggtcaccc agcctccagc 480
tggcaggatt ccctcttcct gtttctcgcc atcttcttct ttttttggt gctcagtatt 540
tga 543

```

<210> 27

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 27

```

gccgtggggt gggaaagtgg gaag gtggag ttttcccag tggcagtgt tagcttggt 60
cctgagaggg agtaccaggt ggaggggtgt ctcaggcacc atcctcctgc cctgggctgc 120
tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
gcntccagca ggatggacct cagccgcagt naggcagcta caggaatcct tagggtctgg 240
ctgggttggg gggtcagctc ctctgcagc tccaggggnt tcaggataac ctccaccctc 300
atccatnttn acatagagga tttcgtcagg ctctggggc aggangcaan gcctttcagt 360
ntgttctoca aatcttccn caactctnta aaacttt 397

```

<210> 28

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(418)

<223> 5' terminal sequence. axl receptor tyrosine
kinase (AXL) gene.

<400> 28

```

ctgaatgaga acatgtccgt gtgtgtggcg gacttcgggc tctccaagaa gatctaca at 60
ggggactact accgccagga ccgtatcgcc aagatgccag tcaagtggat tgccattgag 120
agtctagctg accgtgtcta caccagcaag agcgatgtgt ggtccttcgg ggtgacaatg 180
tgggagattg ccacaagagg ccaaaccoca tatccggggc gtggagaaca gcgagattta 240
tgantatctg cgccagggaa atcgccctgaa gcagcct ncg gactgtcttg gatgggantg 300
ttatgccttg atgttcggcg tncctgggga gcttaaattc ccaggggnc ccgnccaatt 360
ttttacaaag cttnccggga agatttttgg gagnacacac ttttaagggc tttncctt 418

```

<210> 29

<211> 5015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5015)

<223> axl receptor tyrosine kinase (AXL) gene.

<400> 29

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gagtggagtt ctggaggaat gtttaccaga cacagagccc agagggacag cgcccagagc 60
ccagatagag agacacggcc tctactggctc agcaccaggg tccccctccc cctcctcagc 120
tccctcctcg gcccttttaa gaaagagctg atcctctcct ctcttgagtt aaccctgat 180
tgtccagggt gcccttggt ctggcctggt gggcggaggc aaagggggag ccaggggagg 240
agaaagggtt gcccaagtct gggagtgagg gaaggaggca ggggtgctga gaaggcggct 300
gctgggcaga gccggtggca agggcctc cc ctgccgctgt gccaggcagg cagtgccaaa 360
tccggggagc ctggagctgg ggggagggcc ggggacagcc cgcccgcctg cccctcccc 420
cgctgggagc ccagcaactt ctgaggaaag tttggcacc atggcgtggc ggtgccccag 480
gatgggcagg gtcccgtctg cctggtgctt ggctgtgtgc ggctgggctg gcatggcccc 540
caggggcacg caggctgaag aaagtccctt cgtgggcaac ccagggaata tcacagggtg 600
ccggggactc acgggcaccc ttcggtgtca gctccagggt cagggagagc ccccgagggt 660
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cctgggtgag gatgaacagg atgactggat agtggtcagc cagctcag aa tcacctcct 780
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```

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```

<210> 30

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 5' terminal sequence. cathepsin b (CTSB)
gene.

<400> 30

```

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gaatggcaca ccctactggc tgg ttgcaa ctcctggaac actgactggg gtgacaatgg 120
cttcttttaa atactcagag gacaggatca ctgtggaac gaatcagaag tgggtggctgg 180
aattccacgc accgatcagt actgggaaaa gatctaattc gccgtgggcc tgtcgtgcca 240
gtcctggggg gcgagatcgg ggtagaaatg cattttatc ttttaagttc cgtaaggat 300
acaagtttcc agacagggtc tgaaagggan tgggatttng gccaaacatc agacctgttc 360
tttcccaagg gaggaccaag ttcttgggct aacattcccc agcctnttgg ttttaacagt 420
gncaggacag ggcctgtgt 439

```

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<210> 31
<211> 1996
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1996)
<223> cathepsin b (CTSB) gene.

<400> 31
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tggcagctct gggcctccct ctgctgcctg ctggtgttg ccaatgcccg gagcaggccc 240
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agttccccca gtacctcaa gcaagtagct ttccacattt gtcacagaaa tcagagga ga 1620
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ggtttctcca acttga 1996

<210> 32
<211> 492
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(492)

21/292

<223> 3' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 32

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aacaacaga aaaaagaagg aaaaaaagaa aaaaaaatta ttggaaactt catgggtcaa 120
gtggggagag aggaggagga acatggagct aggtctccag gcctctccag agaagtcctc 180
accctcgaag caccctcttg ggggacagca gagccagg ga cagccccccc ccacgccag 240
cctccgtctg agggaagatg ggcagagtca cagtgggtgc gaggggccag aagggttggg 300
aggngggcag gggcgggcgg ggtcacagga agtagttcgg ccacggcttt ctttgggagg 360
gggatncccc gtgtcttctt ttgggggagc agccttcaaa gatgatgaaa tctttttctt 420
gggagatgct tcgttc cagc ttnccaagat tggttncca cattttccca cagcgggtaca 480
agttagtttt tg 492
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<210> 33

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. protein phosphatase 4
(formerly x), catalytic subunit (PPP4C) gene.

<400> 33

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ctggcactta aggttcgcta tcctgatcgc atcacactga tccgggg caa ccatgagagt 120
cgccagatca cgcaggctta tggcttctac gatgagtgcc tgcgcaagta acggctcggg 180
gactgtgtgg cgctactgca ctgagatctt tgactacctc agcctgtcag ccatcatcga 240
tngaaagaat cttctgcgtg caggggggcc tctccccctc catccagacc ctgggatcca 300
gattcggaca atcgaccgaa agcaa gaggt 330
```

<210> 34

<211> 1429

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1429)

<223> protein phosphatase 4 (formerly x),
catalytic subunit (PPP4C) gene.

<400> 34

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gagggggcgg cggccccgac tctgaccgc gccgggggtg ggccatggcg gagatcagcg 120
acctggaccg gcagatcgag cagctgcgtc gctgcgagct catcaaggag agcgaagtca 180
aggccctgtg cgctaaggcc agagagatct tggtagagga gagcaacgtg cagaggggtg 240
actcgccagt cacagtgtgc ggcgacatcc atggacaatt ctatgacctc aaagagctgt 300
tcagagtagg tggcgacgtc cctgagacca actacctctt catggggggac tttgtggacc 360
gtggttctta tagcgtcgaa acgttcctcc tgctgctggc acttaaggt t cgctatcctg 420
atcgcatcac actgatccgg ggcaaccatg agagtcgcca gatcacgcag gtctatggct 480
```


22/292

```
tctacgatga gtgcctgcgc aagtacgggt cgggtgactgt gtggcgctac tgcactgaga 540
tctttgacta cctcagcctg tcagccatca tcgatggcaa gatcttctgc gtgcacgggg 600
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ctaataaaag aagaaaaatg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1429
```

<210> 35

<211> 493

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(493)

<223> 3' terminal sequence. ests (EST T79867)
gene.

<400> 35

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tcccttcccc aagctagctt tggaa taaat ccacttttct tgtaccagac cccactcttg 120
ttaattggac tctacatgtg gnaagcaact aacttgattt tcggttacaa tataatattc 180
aacttcagta aatcaaagac aattttgaaa gaagccaaag ggaaaaaaat gacctgaaga 240
gtcctgttta antttagatt tctgaacaca aatctctggc gactaggact gaagcttgac 300
ctnttcttac ccaggaccn ttcccacctc actagggnac tttggantgg gatatatgtg 360
gggaaactct tgggctttcc ccattgtggc accatttcat atcttatggc aaatggtgcc 420
tcctacctcc cttgggncac tcccngttg gatgggtntt gggggaggag ncctgntggg 480
gntttttccc at 493
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<210> 36

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(354)

<223> 3' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) g ene.

<400> 36

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ggcttccagc ttctctgggc tcaggggcaa tgctcccgtc aagacgtgg ggcagcagca 120
```

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gcagggggag gtnctggggaa aggggggttca gagggcccaga acctcctgct ggtattggga 180
ggcaggaggt ttagcatagc agctctcca g ccaggctcag ccaaaccgg gatggggact 240
aagcgccaag gtccaagaag ccgagcagaa ccctgacatt tggggccatc aggacanagg 300
cacggcagct cccaaggga aggggcacgg ccttngggac angggcacag caac 354

<210> 37

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(336)

<223> 5' terminal sequence. fibroblast growth
factor receptor 4 (FGFR4) gene.

<400> 37

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ggcagcagcg ccctcccaga ggctacott caagcagctg gtggaggcgc tggacaagg 120
ctgctggccg tctctgagga gtacctcgac ctccgcctga ccttcggacc ctattcccc 180
tctggtgggg aacgccagca gcacctgctt cctccagcga ttctgtcttc agccacgacc 240
ccctgccatt ggggattcag ctcttcctt ttgggtctng ggggtgcagac atga gcaagg 300
ctnaagggtt ttgcaaggga catagggtt gtgggc 336

<210> 38

<211> 3015

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3015)

<223> fibroblast growth factor receptor 4 (FGFR4)
gene.

<400> 38

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gctgggagtg aggcggcgga ggagccaggt gaggaggagc caggaaggca gttggtggga 120
agtccagctt gggccctga gagctgtgag aaggagatgc ggctgctgct gg ccctgttg 180
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24/292

```

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gcccttgccc ttgagctgc cgtgctgtg tccgtatgg ccaaatgtca ggttctgct 2760
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cctttcccca cactcccc tgctgctgct gccccagcg cttgacggga gcattggccc 2940
ctgagcccag agaagctgga agcctgccga aaacaggagc aaatggcgtt ttataaa tta 3000
tttttttgaa ataaa 3015

```

<210> 39

<211> 252

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(252)

<223> 3' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 39

```

gtgtgattta ttatgtttaa gattggttta taaggcttaa atatatctgt catagttaac 60
agttaacagc aaataaaggc aactttacaa aatcagtgtt tccatacagt acaggactaa 120
atgtggcaac tgtgcattgg aaaattaata ttctcctaat gcaaatntca aatctgcagc 180
accatttaga agcttcact aaaaactcaa gctgcagtat ttattacang ctctactcng 240
aacacanggc ta 252

```

<210> 40

<211> 382

25/292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(382)

<223> 5' terminal sequence. ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 40

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ctnacnttca aacgganntg gaa ttatttc caaagggtat tggatgaagaa atatgcttcg 60
gaaagaaatg gagttaacgt gataagtggg ccaatcttcg actatgacta tgatggctta 120
catgacacag aagacaaaat aaaacagtac gtggaaggca gttccattcc tgttccaact 180
cactactaca gcatcatcac cagctgtctg gattttactc agcctgccga caagtgtgac 240
ggccctctct ctgtgtcttc ctcatcctcg cctcaccggc ctgacaacga ggagagctgc 300
aatagctcag aggacgnatt caaatgggt agnaggaact catgaaggnt gcacacagct 360
agggtncgtt gacctttgna cc                                     382
```

<210> 41

<211> 2592

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2592)

<223> ectonucleotide
pyrophosphatase/phosphodiesterase 2 (autotaxin)
(ENPP2) gene.

<400> 41

```
atggcaagga ggagctcggt ccagtcgtgt ca gataatat ccctgttcac ttttgccgtt 60
ggagtcaata tctgcttagg attcactgca catcgaatta agagagcaga aggatgggag 120
gaaggtcctc ctacagtgtc atcagactcc ccctggacca acatctccgg atcttgcaag 180
ggcaggtgct ttgaaactta agaggctgga cctcctgatt gtcgctgtga caacttgtgt 240
aagagctata ccagttgtct ccatgacttt gatgagctgt gtttgaagac agcccgctgc 300
tgaggagtga ctaaggacag atgtggggaa gtcagaaatg aagaaaatgc ctgtcactgc 360
tcagaggact gcttgccag gggagactgc tgtaccaatt accaagtgggt ttgcaaagga 420
gagtcgcatt gggttgatga tgactgtgag gaaataaagg ccgcagaatg ccc tgcaggg 480
tttgttcgcc ctccattaat catcttctcc gtggatggct tccgtgcac ataatgaag 540
aaaggcagca aagtcatgcc taatattgaa aaactaagggt cttgtggcac acactctccc 600
tacctgaggg cgggtgtacc aactaaaacc ttctctaact tatacacttt ggccactggg 660
ctatatccag aatcacatgg aattgttggc a attcaatgt atgacctgt atttgatgcc 720
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tggtattacag ccaccaagca aggggtgaaa gctggaacat tcttttggtc tgttgtcatc 840
cctcacgagc ggagaatatt aaccatattg cagtggctca ccctgccaga tcatgagagg 900
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gctaaatatg accccaaagc cattattgcc aatctcacgt gtaaaaaacc agatcagcac 1260
tttaagcctt acttgaaaca gcaccttccc aaacgtttgc actatgccaa caacagaaga 1320
```

26/292

```

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gtttataaga aaccatcagg aaaatgcttt ttccaggag accacggatt tgataacaag 1440
gtcaacagca tgcagactgt tttttaggt tatggcccaa catttaagta caagactaaa 1500
gtgcctccat ttgaaaacat tgaactttac aatgttatgt gtgatctcct gggattgaag 156 0
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cgacctgcag tgctttatcg gactagatat gatattttat atcacactga ctttgaaagt 1860
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aagatgcaca gcagtagggg gcgtgacatt gaacatctca ccagcctgga cttcttccga 2520
aagaccagcc gcagctaccc agaaatcctg aactcaaga catacctgca tacatatgag 2580
agcgagattt aa 2592

```

<210> 42

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog a
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3 (p65)) (RELA) gene.

<400> 42

```

acagatttat tagttcagag tagaaagagc aagagtccaa gtgctttgat tgttcagtaa 60
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cctactatta aggcaactga gaagagggag agcaaggaag tcccagacca aacccttct 180
ggatccnggg ngagagccag tgctgttgcg tggtnntcct tcagccatgg ttgagcaagg 240
aaagagccgg cagagacctc ttagggcag gaaggccagc ccctcaaacg ctggtnttag 300
ggcacagggg acaatgccag tgccatacag gggctggtat ctgggggcgt tattttgatt 360
aagctgtaat gaatccatga tgggaaggac acttgataag gctttntggg gctcaaaggn 420
ctttacctcc agcctgcttc tntctctagg gngagtaccc agaagct 467

```

<210> 43

<211> 2444

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

27/292

<222> (1)..(2444)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog a (nuclear factor of kappa light
polypeptide gene enhancer in b-cells 3 (p65))
(RELA) gene.

<400> 43

```
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tcttcccggc agagcagccc aagcagcggg gcatgcgctt ccgctacaag tgcgaggggc 120
gtcccgcggg cagcatccca ggcgagagga gcacagatac caccaagacc caccaccacca 180
tcaagatcaa tggctacaca ggaccaggga cagtgcgcat ctccctgggtc a ccaaggacc 240
ctctcaccg gcctcaccgc cagcagcttg taggaaagga ctgccgggat ggcttctatg 300
aggctgagct ctgcccggac cgctgcattc acagtttcca gaacctggga atccagtgtg 360
tgaagaagcg ggacctggag caggctatca gtcagcgcac ccagaccaac aacaaccctt 420
tccaagttcc tataagaag cagcgtgggg actacgacct gaatgctgtg cggctctgct 480
tccaggtgac agtgcgggac ccatcaggca ggccccctcg cctgccgcct gtcctttctc 540
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gaaactcttg cagctgcctc ggtggggatg agatcttctt actgtgtgac aagggtgcaga 660
aagaggacat tgaggtgtat ttacggggac caggctggga ggcccgaggc tccttttcgc 720
aagctgatgt gcaccgacaa gtggccattg tgttccggac ccctccctac gcagacccca 780
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caggagggcat agtttttagt gaacaatcaa agcacttgga ctcttgcctt ttctactctg 2400
aactaataaa gctgttgcca agctggacgg cagcagctcg tgcc 2444
```

<210> 44

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(381)

28/292

<223> 5' terminal sequence. il2 -inducible t-cell
kinase (ITK) gene.

<400> 44

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aactctttcc tttggttggtg ctaagaggtg atgcccaagg tgcaccacct ttcaagaact 60
ggatcatgaa caactttatc ctcttggaag aacagctcat caagaaatcc caacaagaga 120
agaacttctc cctcgaactt taaagtccgc ttctttgtgt taaccaaagc cagcctgg ca 180
tactttgaag atcgtcatgg gaagaagcgc acgctgaagg ggtccattga gctctcccga 240
attcaaatgt gttgaggttg tgaaaagtga catcagcatc ccatgccact attaaatacc 300
cgttttcagg tnggtgcatg acaacttacc tcctnttatg gtgtttgntt ccagntcgtg 360
aggaggccgg ncagcgttng g                                     381
```

<210> 45

<211> 6381

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6381)

<223> il2-inducible t-cell kinase (ITK) gene.

<400> 45

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aatatatcca acacttacaa aaagtgatat gataaagaat ataaagtact agtttccttt 180
taacacttca aaagatatgt atatatactt ttttttacaa gtaacatcac aaatgctcac 240
atcttcacat gctcttaaag tattatttgt actcagtgtg aggctattat cgtttttcat 300
acataaaatt ttctagctct gtaacacaat gcaattttta atccattcag taagttcaac 360
cccaaagttg ccgcttccca gcattaagac atgcaccac ccctcttcta agattttcta 420
aacttgatatt tcggggagaa agacctct tt taaaaaataa tccaattagt gggagagtaa 480
atggctgaca ttagtagcaa aaccttagtt atctgaaaat aacatattgg aaatgagaca 540
ttattaggat tttaacaaa caatagcatt tagacataaa gtaggaagca aaatacagta 600
aacagaaata gtgtagccaa atatcattct ctacagctac ctttaagtaa agacaaaaca 660
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```

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30/292

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ctgtacagcc tgacactgta tgggctgcga ggacccaca aggcagacag catccaggga 11580
accgccccga cctcagccc agttctggag agccccctg acctcaatt cagtgaatc 11640

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```

agggagacct cagccaaggt caactggatg cccccacct cccgggcgga cagcttcaaa 11700
gtctcctacc agctggcgga cggaggggag cctcagagtg tgcaggtgga tggccag gcc 11760
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agccagggtc cttcaccacc cagccgctgg aggaagcct ctctgccagc gatctcgag 13200
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gtaccgg 13268

```

<210> 48

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 3' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 48

```

ttttgcagct tgtgcacttc ttttattatt aaatatataa gcagcttcct atcttttaaa 60
tagatattta aatgacttta tataaaataa ttcaccactt ccaagtataa aaacaaaatc 120
tcacagtgcg tgancaatgt cctctc ttga cttctcagag aacagaagg gttcctgagc 180
aggtagcctg gggggacacc agaggngcct ctggggctcc tcctgctctg atgccaccaa 240
gtgctcaaaa agagcttctg cagtggggtt gggattgctt ttttgacctt taaaatatta 300
tatgtttaag gtaggggggg atgaaggggg gaatgccctt tttatttttc ttcccatttt 360
aaaaatatgt gttttctagg catccaaata tagggggctg tggcctggga gggctaggcc 420
ccctttgccca ggttcact 438

```

<210> 49

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 49

```
ggcacgagggc gagctctgac tgaagatggg cctttgaaat ataggtatgc acctgaggtt 60
gggggaggggt ctgcactccc aaaccccagc gcagtgtcct ttccttgc tg ccgacagaac 120
ctggggctga gcaggttatc cctgtcagga gccctgggac tgggctgcat ctacagccca 180
cctggcatgg tatecagctc ccatccactt cttcaccctt ctttcctcct gacctgggt 240
caacagtgat ggacctcca actcttcacc caccctctt accattcacc tctaaaccag 300
gggaagccag gggtngggag agcant cagg gagagccagg gcttcagttt tccaattgct 360
ggggangggc ttccattttn tggggccagg 390
```

<210> 50

<211> 2475

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2475)

<223> colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 50

```
agccgctctc cgcaccccag gacagcgggt cggccctcgg ccggggcgcc cactccgag 60
caccacagca gcgagcgagc gagcgagggc ggccgacgag cccggccggg acccagctgc 120
ccgtatgacc gcgcggggcg ccgcggggcg ctgccctccc acgacatggc tgggctccct 180
gctgttgttg gtctgtctcc tggcgagcag gagtatcacc gaggaggtgt cggagtactg 240
tagccacatg attgggagtg gacacctgca gtctctgcag cggctgattg acagtcagat 300
ggagacctcg tgccaaatta catttgagtt tgtagaccag gaacagttga aagatccagt 36 0
gtgtacactt aagaaggcat ttctcctggt acaagacata atggaggaca ccatgcgctt 420
cagagataac acccccaatg ccatcgccat tgtgcagctg caggaactct ctttgaggct 480
gaagagctgc ttcaccaagg attatgaaga gcatgacaag gcctgcgtcc gaactttcta 540
tgagacacct ctccagttgc tggagaaggt caagaatgtc ttaaatgaaa caaagaatct 600
ccttgacaag gactggaata ttttcagcaa gaactgcaac aacagctttg ctgaatgctc 660
cagccaagat gtggtgacca agcctgattg caactgcctg taccctaaag ccacccctag 720
cagtgaacct gcctctgtct cccctcatca gccctcgcgc ccctccatgg cccctgtggc 780
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agcaagtga ggggcagcca ggcccctgcc ccgttttaac tccgttcctt tgactgacac 1560
acatgagagg cagtcagagg gatcctccag cccgcagtc caggagtctg tcttccacct 1620
gctgggtgcc agtgtcatcc tggctcttgc ggccgtcgga ggcctcttg t tctacaggtg 1680
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gaggcggcgg agccatcaag agcctcagag agcggattct cccttgagc aaccagagg 1740
cagccccctc actcaggatg acagacaggt ggaactgcc a gtgtagagg aattctaaga 1800
cccctcacca tcctggacac tctcgtttgt caatgtccct ctgaaaatgt gacgccagc 1860
cccggacaca gtactccaga tgttgtctga ccagctcaga gagagtacag tgggactgtt 1920
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taactttttt aaccaaagtg cagtttatgt tcacctttgt taaagccacc ttgtggttc 2160
tgcccatcac ctgaacctac tgaagtgtg tgaatccta attctgtcat ctccgtagcc 2220
ctcccagttg tgctcctgc acattgatga gtgcctgctg ttgtctttgc ccatgttgtt 2280
gatgtagctg tgacctatt gttcctcacc cctgccc ccc gccaaccca gctggccac 2340
ctcttcccc tcccaccaa gccacagcc agccatcag gaagccttc tggcttctcc 2400
acaacattt gactgtctt tcagtcatgc cccctgctt tttgtattg gctaatagta 2460
tatcaatttg cactt                                     2475

```

<210> 51
 <211> 397
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(397)
 <223> 3' terminal sequence. villin 2 (ezrin)
 (VIL2) gene.

```

<400> 51
atcngttgaa tagttgattc catacatttc cagg tcttga gcaatcttca ggtattccaa 60
catagcatta tctttgagca tcccacgggtg ttccgcatgc cacacctgga tccggtcctc 120
ccactggtcc ctggttaagtt tgtgtggtc catcactctt tgagggatca nccgctcaga 180
gctgaggtag ccagacttgt gcacttcttt gttgtagtcc ccaaacttgg cctgcacagc 240
gtagggaccc caagagcacg gcagtctcag ggggggcagt agatctcatc gctaagggat 300
tcctttcctt cacttnggag ggaggaaaag tttctgggt gatgtcctgg ggatgagctt 360
ccttcagcca catctttcag ggnaggact ttnggcc                                     397

```

<210> 52
 <211> 468
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(468)
 <223> 5' terminal sequence. villin 2 (ezrin)
 (VIL2) gene.

```

<400> 52
ggacgaggca gggcggggc gcgtctaaag ggttctgctc tgactccagg ttgggacagc 60
gtcttcgctg ctgctggata gtcgtgtttt cggggatcga ggatactcac cagaaaccga 120
aaatgccgaa accaatcaat gtccgagtta ccacatgga tgcagagctg gagtttgcaa 180
tccagccaaa tacaactgga aaacagcttt ttgatcaggt ggtaaagact atcggcctcc 240
gggaagtgtg gtactttggc ctccactatg tggatnaata aaggatttcc tacctgg gct 300
gaagctggat aagaaggtgt ctgcccagga ggtcaggaag gagaatcccc tccagttcaa 360

```

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gttccggggc caagttctac cctgaagatg tgggctgagg agctcattcc agggacattc 420
accagaaat tttntttcnt ccaagtgaag gaagggattc ttaggcgn 468

<210> 53

<211> 3064

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3064)

<223> villin 2 (ezrin) (VIL2) gene.

<400> 53

aggcagggcg ggcgggcgct ctaagggttc tgctctgact ccaggttggg acagcgtctt 60
cgctgctgct ggatag tcgt gttttcgggg atcgaggata ctcaccagaa accgaaaatg 120
ccgaaaccaa tcaatgtccg agttaccacc atggatgcag agctggagtt tgcaatccag 180
ccaaatacaa ctggaaaaca gctttttgat caggtggtaa agactatcgg cctccgggaa 240
gtgtggtact ttggcctcca ctatgtggat aataaaggat ttctacctg gctgaagc tg 300
gataagaagg tgtctgcccc ggaggtcagg aaggagaatc ccctccagtt caagttccgg 360
gccaaagttct accctgaaga tgtggctgag gagctcatcc aggacatcac ccagaaactt 420
ttcttctctc aagtgaagga aggaatcctt agcgaatgaga tctactgccc ccctgagact 480
gccgtgctct tggggctcta cgctgtgcag gccaaag tttg gggactacaa caaagaagtg 540
cacaagtctg ggtacctcag ctctgagcgg ctgatccctc aaagagtgat ggaccagcac 600
aaacttacca gggaccagtg ggaggaccgg atccaggtgt ggcattgcga acaccgtggg 660
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ggaatcaact atttcgagat aaaaaacaag aaaggaacag acctttggct tggagttgat 780
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cttgatatt ttttagttc ttttttttt ggcttaacag ttttagaata cattgtactt 2520
atacacctta ttaatgatca gctatatac atttatatac aagtataat acagatttgt 2580

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```

aacattagtt ttaaaaaggg aaagttttgt tctgtatatt ttgttacctt ttacagaata 2640
aaagaattac atatgaaaaa cctctaaaac catggcactt gatgtga tgt ggcaggaggg 2700
nagtgggtgga gctggacctg cctgctgcag ctgcagtcac gtgtaaacag gattattatt 2760
agtgttttat gcatgtaatg gactatgcac acttttaatt ttgtcagatt cacacatgcc 2820
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gcccaactcat tccttctcgt gcactgcttt ctcttcaca gctaagatgc catgtgcagg 3000
tggtatccat gccgcagaca tgaaataaaa gctttgcaaa ggcaaagaaa aaaaaaaaaa 3060
aaaa
3064

```

<210> 54

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 3' terminal sequence. adenomatosis polyposis coli (APC) gene.

<400> 54

```

tgcataaata ccaatttttc cctgatgtaa gtttagtcag ttataatct agaatgatt 60
gataacagca atatatcata tttctatct gtagtggtca ttattttaag acaagcaata 120
attaaaggaa gttgggatgg gatgctactt taaatacatg taaaacatac tgtacaaaca 180
tacttggtt tactattttt ttctaacca tcaagagtgc ctcccaaat aa gnccagtg 240
aagacaaagt atactatcaa atatgggctt ccnggaacaa aaaccctctt aacaagggt 300
ccaaacccta ttacacaaaa tttcccgggt cttttaaggt ttccatttgg aaacacaaat 360
gtctatatgg ccggttggtg attancatgg ggnntttctt ggnnttcctt cttccnct 420
cttttaacc ggtgg
435

```

<210> 55

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. adenomatosis polyposis coli (APC) gene.

<400> 55

```

agaaaaatgaa ttttctccca caaatagtag ttctcagacc gtttcctcag gtgctacaaa 60
tggtgctgaa tcaaagactc taatttatca aatggcacct gctgtttcta aaacagagga 120
tggttgggtg agaattgagg actgtcccat taacaatcct agatctggaa gatctccac 180
aggtaatact cccccggtga ttg acagtgt ttcaaaaaag gcaaatccaa acattaaaga 240
ttcaaaagat aatcagggca aaacaaaatg tggggtaatn ggcagtgttc ccatgncgta 300
ccgtggggtt tnggaaaatc gcctggaact cttttatttc aggtgggatg cccctgacca 360
aaaaggganc tttnggttna aaccggggnc aaattattcc tgttccctgt ttcc 414

```

<210> 56

<211> 10383

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(10383)

<223> adenomatosis polyposis coli (APC) gene.

<400> 56

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agttgttaaa gcaagttgag gcaactgaaga tggagaactc aaatcttcga caagagctag 120
aagataattc caatcatctt acaaaaactgg aaactgaggc atctaatatg aaggaagtag 180
ttaaacaact acaaggaagt attgaagatg aagctatggc ttcttctgga cagattgatt 240
tattagagcg tcttaaagag ctttaacttag atagcagtaa ttccctgga gtaaaaactgc 300
ggtaaaaaat gtccctcctg tcttatggaa gccgggaagg atctgtatca agccgttctg 360
gagagtgcag tccgtttcct atgggttcat ttccaagaag aggggttgta aatggaagca 420
gagaaagtac tggatattha gaagaacttg agaaagagag gtcattgctt cttgc tgate 480
ttgacaaaga agaaaaggaa aaagactggg attacgctca acttcagaat ctcactaaaa 540
gaatagatag tcttctttha actgaaaatt ttctcttaca aacagatatg accagaaggc 600
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cagccaagtgt tttgagttct agtagcacac actctgcacc tcgaaggctg acaagtcata 960
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acaacatcat tcactcacg cctgatgaca agagaggcag gcgtgaaatc cgagtccctc 1260
atcttttggg acagatacgc gcttactgtg aaacctgttg ggagtggcag gaagctcatg 1320
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<210> 57

<211> 404

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(404)

<223> 5' terminal sequence. mucin 1, transmembrane
(MUC1) gene.

<400> 57

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ctatgagcga gtacccacc taccacacc atggggcgct atgtgcccc taggcagtac 300
cgatcgtagc ccctatgaga aggttttng caggtaatng gttggcagca gcttttttta 360
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<210> 58

<211> 1721

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1721)

<223> mucin 1, transmembrane (MUC1) gene.

<400> 58

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<210> 59

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 3' terminal sequence. insulin-like growth
factor 2 (somatomedin a) (IGF2) gene.

<400> 59

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<210> 60

<211> 410

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(410)

<223> 5' terminal sequence. insulin-like growth
factor 2 (somatomedin a) (IGF2) gene.

<400> 60

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<210> 61
<211> 1356
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1356)
<223> insulin-like growth factor 2 (somatomedin a)
(IGF2) gene.

<400> 61
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ttctgtttct ctccgtgctg ttctctcccg ctgtgcgcct gccgcctct cgctgtcttc 180
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<210> 62
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(474)
<223> 3' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 62
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<210> 63

<211> 457

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(457)

<223> 5' terminal sequence. egf-like module
containing, mucin-like, hormone receptor-like
sequence 1 (EMR1) gene.

<400> 63

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gntttgcaan tttttcaan ttccagagtt ttttgaggna caggacccaa nttcantggg 420
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<210> 64

<211> 3149

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3149)

<223> egf-like module containing, mucin-like,
hormone receptor-like sequence 1 (EMR1) gene.

<400> 64

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<210> 65

<211> 412

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(412)

<223> 3' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 65

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tgaaggttta cagactggc aaggaaggac gaacagagag aatgggtct gaggggtcac 120
atcccgtgga ggggtggcgg gctcctggcc tcgtctgggt gaggttggga gcctcgctgg 180
ggctgcggtc ccagagcttc ggcaaagcca ccaggccttg gggagcaggg ctttggcaag 240
caggccgcct cgga gaaaaa caatgactaa ctatcctga cagggcagtt ggggagactt 300
taggacaggn ttcaacattc agatgggctt ggaccncctt tttcattnc ggccaaggaa 360

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ccccggggcn aggggngaaa gcaattncaa agccttttagg aaatttcaat tt

412

<210> 66
<211> 442
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(442)
<223> 5' terminal sequence. k1aa0427 gene product
(K1AA0427) gene.

<400> 66
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<210> 67
<211> 5737
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5737)
<223> k1aa0427 gene product (K1AA0427) gene.

<400> 67
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<210> 68

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 68

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gagtggggaa agacatgaag gggatttggg aacagatccg taaaaataa cctgttntgg 360
aaattcacca caggcca 377

```

<210> 69

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(323)

<223> 5' terminal sequence. spleen tyrosine kinase
(SYK) gene.

<400> 69

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gaataatctc aagaatcaaa tcatactcct tcccaaagcc tggccacaga aagtcctccc 120
ctgcccaagg gaaccncaa gagagtactg tgtcattcaa tccgtatgag gccaggaact 180
tgcacccggg gcttgacgga caaaggggcc cca gaggagg aagccctacc cntgggacac 240

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agaggtgtta cggaggagcc cntacggcgg gaccccgagg gagnttcagg gcccaagggn 300
gtttttactt gggggaccga aag 323

<210> 70

<211> 2541

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2541)

<223> spleen tyrosine kinase (SYK) gene.

<400> 70

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ggccatgaga ctgatccctg gccactgaaa agctttctg aca ataaaaa tgttttgagg 2520
ctttaaaaaa aaaaaaaaaa a 2541

<210> 71
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. interleukin 7 receptor
(IL7R) gene.

<400> 71
taacatcttt gtaagaaacc aagaaaaaat ttaaattgga gtttcaatcc tgaaagtttc 60
ctggactgcc agattcatag ggtggatgac attcaagcta gagatgaagt ggaaggtttt 120
ctgcaagata cgtttctctca gcaactagaa gaatctga ga agcagaggct tngaggggat 180
gtgcagagcc ccaactgccc atctgaggat gtagtcatca ctccaggaaa gctttgggaa 240
ggagattcat cctcacatg cctgggctng ggaatgttca gtgcattgta cgcccctatt 300
tttctccttt t 312

<210> 72
<211> 1658
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1658)
<223> interleukin 7 receptor (IL7R) gene.

<400> 72
ctctctctct atctctctca gaatgacaat tctaggtaca acttttggca tgggt tttttc 60
tttacttcaa gtcgtttctg gagaaagtgg ctatgctcaa aatggagact tggaagatgc 120
agaactggat gactactcat tctcatgcta tagccagttg gaagtgaatg gatcgagca 180
ttcactgacc tgtgcttttg aggaccaga tgtcaacacc accaatctg aatttgaaat 240
atgtggggcc ctctggagg taaagtgcct gaa tttcagg aaactacaag agatatattt 300
catcgagaca aagaaattct tactgattgg aaagagcaat atatgtgtga aggttggaga 360
aaagagtcta acctgcaaaa aaatagacct aaccactata gttaaacctg aggctcctt 420
tgacctgagt gtcactctatc gggaaggagc caatgacttt gtggtgacat ttaatacatc 480
acacttgcaa aagaagtatg taaaagtttt aatgcatgat gtagcttacc gccaggaaaa 540
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aaagctccaa ccggcagcaa tgtatgagat taaagttcga tccatccctg atcactattt 660
taaaggcttc tggagtgaat ggagtccaag ttattacttc agaactccag aga tcaataa 720
tagctcaggg gagatggatc ctatcttact aaccatcagc attttgagtt tttctctgt 780
cgctctgttg gtcactctgg cctgtgtgtt atggaaaaaa aggattaagc ctatcgatg 840
gcccgctctc cccgatcata agaagactct ggaacatctt tgtaagaaac caagaaaaaa 900
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tggaagaat gggcctcatg tgtaccagga cctcctgctt agccttggga ctacaaacag 1260
cacgctgccc cctccatttt ctctccaatc tggaatcctg acattgaacc cagttgctca 1320

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gggtcagccc attcttactt ccctgggatac aaatcaagaa gaagca tatg tcaccatgtc 1380
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aattagcaaa accccactac acagtctgca agattctgaa acattgcttt gaccactctt 1560
cctgagttca gtggcactca acatgagtca agagcatcct gcttctacca tgtggatttg 1620
gtcacaaggt ttaaggtgac ccaatgattc agctattt 1658

<210> 73
<211> 236
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(236)
<223> 3' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 73
taaaaaaat agaaaaaat caactttaaa aagcaaaatg tacttaaata aaaaaaatta 60
gggtttatag tacctataat actaggnact atatactagg attgaaa ttc tgtgtaactg 120
ctataaacgt tttattaaag ttatttacat ttaatgggca atatttacag aggaaacatt 180
gtgtaaactt taaaattttt taaaanccaa ttcttaaata ccaaatctgt taaggg 236

<210> 74
<211> 413
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(413)
<223> 5' terminal sequence. v-myc avian
myelocytomatosis viral oncogene homolog (MYC)
gene.

<400> 74
acgtctccac acatcagcac aactacgcag cgcctccctc cactcggaag gactatcctg 60
ctgccaagag ggtcaagttg gacagtgtca gagtccctgag acagatcagc aacaaccgaa 120
aatgcaccag cccaggttcc tcggacaccg aggagaatgt caagaggcga acacacaacg 180
tcttgggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 240
atcccggagt tgggaaaaca atgaaaaggc cccaaggta gttattcctt taa aaaagcc 300
acagcntaca tcctgttccg ttccaaggca ggaggagacc aaaagttcat tttnttgaag 360
gagggnnttt tttccgggn aacgacgag aaccattttn aaacacaant ttt 413

<210> 75
<211> 2121
<212> DNA/RNA
<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> v-myc avian myelocytomatosis viral oncogene
homolog (MYC) gene.

<400> 75

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ataaaagccg gttttcggg ctttatctaa ctcgctgtag taattccagc gagaggcaga 180
gggagcgagc gggcgccgg ctagggtgga agagccggg gagcagagct gcgctgcggg 240
cgtcctggga agggagatcc ggagcgaata gggggcttcg cctctggccc agccctcccg 300
cttgatcccc caggcca gcg gtccgcaacc cttgcgcat ccacgaaact ttgccatag 360
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acgcggggag gctattctgc ccatttggg acacttccc gcgctgcca ggaccgctt 480
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cagcagcctc ccgcgacgat gccctcaac gttagcttca ccaacaggaa ctatgacctc 600
gactacgact cgtgcagcc gtatttctac tgcgacgag aggagaactt ctaccagcag 660
cagcagcaga cggagctgca gccccggcg ccacgagag atatctggaa gaaattcgag 720
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agcttgtagc tgcaggatct gagcgccgc gcctcagagt gcatcgacc ctcggtggtc 1140
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tctgaagag acttggtgcg gaaacgacga gaacagttga aa cacaaact tgaacagcta 1860
cggaactctt gtgcgtaagg aaaagtaagg aaaacgattc cttctaacag aaatgtcctg 1920
agcaatcacc tatgaacttg tttcaaagtc atgatcaaat gcaacctcac aaccttggct 1980
gagtccttag actgaaagat ttagccataa tgtaaaactgc ctcaaattgg actttgggca 2040
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attgttttta aaaaatttta a 2121
```

<210> 76

<211> 260

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(260)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

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<400> 76

```

tcacagcact agagaccctg ttaaataggg gatatgagtc agaatggctt attcacagat 60
ggggtccaga ttcagtgggt ggaacacaga caccacagtg agtcctttg caaagtggca 120
aacataattt tgctttctgc cttcaaaaac atatatccat cgcgtttagg cttcatgata 180
ctgctcctgc aaaaatgcaa gtcgaaaggg actgcaggga ctctcgctgg ggggccctgt 240
gagcatcgag cagggtcttt                260

```

<210> 77

<211> 409

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(409)

<223> 5' terminal sequence. gata -binding protein 3
(GATA3) gene.

<400> 77

```

cattctgggt catagatggc atcttttcac tgtgttctca cattggtgga aaggaagaac 60
tctggtttct tcacttcctt ataagggcac caatcttatt cagagggtc tcaccctcga 120
aataatcacg tcctcaaaac cccaccttc taatattcta ataccatcac gtgagggtt 180
aggtttcaac ataagaattc ggtggtggtn gggttnggg gagagggaaa caaacatcca 240
gaccagaaac cgaaaaatgt ctagcaaadc caaaaagtgc aaaaaagt gc atgactcact 300
ggaggacttc cccaagganc agctncgttt taaccggggc cgcccttttc caggacacat 360
gttccttccc tggnggccac atnttgncc ttnaggccan tccagggca                409

```

<210> 78

<211> 2365

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2365)

<223> gata-binding protein 3 (GATA3) gene.

<400> 78

```

tcccagcctt cccatcccc caccgaaagc aaatcattca acgacccccg accctccgac 60
ggcaggagcc ccccgacctc ccaggcggac cgcccttccc tcccgcgcg ggttccgggc 120
ccggcgagag ggcgcgacga cagccgaggc catggagggt acggcggacc agccgcgctg 180
ggtgagccac caccaccccg ccgtgctcaa cgggcagcac ccggacacgc accaccggg 240
cctcagccac tcctacatgg acgcggcgca gtaccgcgtg ccggaggagg tggatgtgct 300
ttttaacatc gacggtcaag gcaaccacgt cccgccttac ta cggaaact cggtcagggc 360
cacggtgcag aggtaccctc cgaccacca cgggagccag gtgtgccgcc cgcctctgct 420
tcattgatat ctaccctggc tggacggcgg caaagccctg ggcagccacc acaccgcctc 480
ccctggaat ctcagccctt tctccaagac gtccatccac cacggctccc cggggccct 540
ctccgtctac ccccggcctt cgtcctctc cttgtcggg ggccacgcca gcccgacct 600
cttcacctc cgcgccccc cgcgaagga cgtctcccc gaccatcgc tgtccacct 660
aggtcgggcc ggctcggccc ggcaggacga gaaagagtgc ctcaagtacc aggtgccct 720
gcccgacagc atgaagctgg agtcgtccca ctcccgtagc agcatgaccg ccctgggtgg 78 0
agctcctcgt tcgaccacc accccatcac cacctaccg ccctacgtgc ccgagtacag 840
ctcgggaatc ttcccccca gcagcctgct gggcggtcc cccaccggt tcggatgcaa 900

```

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```

gtccaggccc aaggcccggg ccagcacagg cagggagtgt gtgaactgtg gggcaacctc 960
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caaatccaaa aagtgcacaaa aagtgcacat ctactggag gacttcccca agaacagctc 1320
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gccactttgc aaaggagctc actgtggtg t ctgtgttcca accactgaat ctggacccca 1680
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tattgcatct gggtagctgt aaggcatgaa ggatgccaag aagtttaagg aatatgggag 1860
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tgtttgtatg tataattcaa agcaccaaaa taagaaaaga tgtagattta tttcatcata 2220
ttatacagac cgaactgttg tataaattta tttactgcta gtcttaagaa ctgctttcctt 2280
tcgtttgttt gtttcaa tat tttccttctc tctcaatttt cggttgaata aactagatta 2340
cattcagttg gcaaaaaaaaa aaaaa 2365

```

<210> 79

<211> 328

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(328)

<223> 3' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 79

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ttgtatnttt naaataatct ttattgtcac tagtataaaa cagagcagat caactggcct 60
ctcggctctgt acaaagtgtg gggcgtgaaa ccgctgggct gccccactt ctcccataat 120
tccctgcctt agagcagcag ctccagagct aggagaagga gagggggcca cccaaggcct 180
tcccttgagg agaggggtca ggagtggact ggagtggggg ctgttttcta tctgaggagg 240
gcaaaagaagc agaggagaaa actggagtgg cggaaccctc ccgntcctca tcccgtcccc 300
tgtggccgat cccanagtcc actnggat 328

```

<210> 80

<211> 428

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(428)

<223> 5' terminal sequence. growth factor
receptor-bound protein 7 (GRB7) gene.

<400> 80

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ggctccccac ccttgagaag tgcctcagat aataccctgg tggccatgga cttctctggc 60
catgctgggc gtgtcattga gaacccccgg gaggtcttga gtgtggccct ggaggaggcc 120
caggcctgga ggaagaagac aaaccaccgc ctacgcctgc ccatgccagc ctccggacga 180
gcctcagtgc agccatccac cgcacccaac tctggttcca cgggcgcatt tcccgtgagg 240
agagccagcg tttattggga cagcagggct tngtagacgg cctgttctctg ggtccgggag 300
agtcagcggg aacccccagg ggtttttcct ctttttnttg ccaccttgca gaaagtgaag 360
cnttattttc attccttgcc gagcgaagga ggaagggccg cttttatttt aagcattggt 42 0
tgattggc 428
```

<210> 81

<211> 2205

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2205)

<223> growth factor receptor-bound protein 7
(GRB7) gene.

<400> 81

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cacagggtc cccccgcct ctgacttctc tgtccgaagt cgggacaccc tctaccacc 60
tgtagagaag cgggagtgga tctgaaataa aatocaggaa tctgggggtt cctagacgga 120
gccagacttc ggaacgggtg tctgtctact cctgtctggg ctcctccagg acaaggga c 180
acaactggtt cgttaagcc cctctctcgc tcagacgcca tggagctgga tctgtctcca 240
cctcatctta gcagctctcc ggaagacctt tggccagccc ctgggacccc tctggggact 300
ccccggcccc ctgatacccc tctgcctgag gaggtaaaga ggtcccagcc tctcctcatc 360
ccaaccacgc gcaggaaact tcgagaggag gagagggc gtg ccacctccct cccctctatc 420
cccaaccctt tccctgagct ctgcagtcct ccctcacaga gcccaattct cggggggccc 480
tccagtcaa gggggctgct cccccgcgat gccagccgcc cccatgtagt aaagggttac 540
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tgccaccccc acctagcact ggagcggggt ttggaggacc acgagtccgt ggtggaagtg 720
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ctcgatgcac aactgggtat atcccatgaa gacctcatcc agaacttcct gaatgctggc 900
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acgcgggtgg cctctgacc aggcgtgga ctggctcatg cctcagccc ccttcaggct 1860
gcccccgcc cctccacca tccagtggac tctggggcgc ggccacaggg gacgggatga 1 920
```

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ggagcgggag ggttccgcca ctccagtttt ctctctctgt tctttgctc cctcagatag 1980
aaaacagccc ccactccagt ccactcctga cccctctcct caagggaagg ccttgggtgg 2040
ccccctctcc ttctcctagc tctggagggt ctgctctagg gcagggaatt atgggagaag 2100
tgggggcagc ccaggcgggt tcacgcccc cacttt gtac agaccgagag gccagttgat 2160
ctgctctggt ttatactagt gacaataaag attatttttt gatac 2205

<210> 82

<211> 313

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(313)

<223> 5' terminal sequence. topoisomerase (dna) ii
beta (180kd) (TOP2B) gene.

<400> 82

gaaatttgac agtaatgaag aagattctgc ttctgttttt tcaccatcat ttggtctgaa 60
acagacagat aaagttccaa gtaaaacggt agctgctaaa aagggtatgt acttataatt 120
gattgagtta agcattgg at agagatagtt aatgtaaaag gaaatgtaat ttaatttgaa 180
actatttgca tttttttatc ataaaacaat taaggaagta taagtgttta taaggaggac 240
ctctcgtttt ctagccatct gagggcggtta ataaatttct gtaggactta ntttaaagct 300
gttgantttt taa 313

<210> 83

<211> 4866

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4866)

<223> topoisomerase (dna) ii beta (180kd) (TOP2B)
gene.

<400> 83

atggccaagt cgggtggctg cggcgcggga gccggcgtgg gcggcgcaa cggggcactg 60
acctgggtga acaatgctgc aaaaaaagaa gagtcagaaa ctgccacaa aaatgattct 120
tcaaagaagt tgtctgttga gagagtgtat cagaagaaga cacaacttga acacattctt 180
cttcgtctctg atacatatat tgggtcagtg gagccattga cgcagttcat gtgggtgt at 240
gatgaagatg taggaatgaa ttgcaggag gttacctttg tgccaggttt atacaagatc 300
tttgatgaaa ttttggttaa tgctgctgac aataaacaga gggataagaa catgacttgt 360
attaaagtgt ctattgatcc tgaatctaac attataagca tttggaataa tgggaaaggc 420
attccagtag tagaacacaa ggtagagaaa gtttat gttc ctgctttaat ttttgacag 480
cttttaacat ccagtaacta tgatgatgat gagaaaaaag ttacaggttg tcgtaatggt 540
tatgggtgcaa aactttgtaa tattttcagt acaaagttaa cagtagaaac agcttgcaa 600
gaatacaaac acagttttta gcagacatgg atgaataata tgatgaagac ttctgaagcc 660
aaaattaaac attttgatgg tgaagattac acatgcataa cattccaacc agatctgtcc 720
aaatttaaga tggaaaaact tgacaaggat atttggtccc tcatgactag aagggcata 780
gatttggtctg gttcgtgtag aggggtcaag gtcattgtta atggaaagaa attgcctgta 840
aatggatttc gcagttatgt agatctttat gtgaaagaca aattggatga aactgg ggtg 900
gccctgaaag ttattcatga gcttgcaaat gaaagatggg atgtttgtct cacattgagt 960

gaaaaaggat tccagcaaat cagcttttga aatagtattg caactacaaa aggtggacgg 1020
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 aatgatgctg gtggtaaaca ttccctggag tgtacactga tattaacaga gggagactct 1440
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 ccactcagg gcaaaattct taatgtacgg gaagcttctc ataaac agat catggaaaat 1560
 gctgaaataa ataattattat taaaatagtt ggtctacaat ataagaaaag ttacgatgat 1620
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 gatggttctc acataaaagg cctgcttatt aatttcatcc atcacaattg gccatcactt 1740
 ttgaagcatg gttttcttga agagttcatt actcctattg taaaggcaag caaaaataag 1800
 caggaaactt cctctacag tattcctgaa ttgacgaat ggaaaaaaca tatagaaaac 1860
 cagaaagcct ggaaaataaa gtactataaa ggattgggta ctagtacagc taaagaagca 1920
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 gatgatgctg ccattacctt ggcathtagt aagaagaaga ttgatgacag aaaagaatgg 2040
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 ttatgtgta ctgcaacaaa gcatttgact tataatgatt tcatcaaca ggaattgatt 2160
 ctcttctcaa actcagacaa tgaagatctc atac catctc ttgttgatgg ctttaaacct 2220
 ggccagcgga aagttttatt tactgtttc aagaggaatg ataaacgtga agtaaaagt 2280
 gccagttgg ctggctctgt tgctgagatg tggcttctc atcatggaga acaagcattg 2340
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 cagcctattg gtcagtttgg aactcggctt catgggtggca aagatgctgc aagccctcgt 2460
 tatatttca caatgttaag cactttagca aggtactttt ttctgtctgt ggatgacaac 2520
 ctcttaagt ccttttatga tgataatcaa cgtgtagagc ctgagtggta tattcctata 2580
 attcccatgg ttttaataaa tgggtgctgag ggcattggta ctggatgg gc ttgtaaaacta 2640
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 cctcatocca tgcttccaaa ctacaaaaac tttaaaggca cgattcaaga acttgggtcaa 2760
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 catatgggat gtctgaagaa atatgaaact gtgcaagaca ttctgaaaga attctttgat 3120
 ttacgattaa gttattacgg ttacgtaag gagtggcttg tgggaatggt gggagcagaa 3180
 tctacaaagc ttaacaatca agcccgtttc atttttagaga agatacaagg gaaaattact 3240
 atagagaata ggtcaaagaa agatttgatt caaatg ttag tccagagagg ttatgaatct 3300
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 aaccagcatg atgatagttc ctccgattca ggaactcctt caggcccaaga ttttaattat 3420
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 aaagaggatt tagcggcatt tgttgaagaa ctggataaag tggaaatctca agaacgagaa 3600
 gatgttctg ctggaatgtc tggaaaagca attaaaggta aagttggcaa acctaaagggtg 3660
 aagaaactca agttggaaga gacaatgcc tcaccttatg gcagaagaat aattcctgaa 3720
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 gaagaccta aatacacatt tgatttctca gaagaagag atgatgatgc tgatgatgat 414 0
 gatgatgaca ataattgattt agaggaattg aaagttaaag catctcccat aacaaatgat 4200
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 aatctcttct catttcttcc atattctcag aagtcaga ag atgattcagc taaatttgac 4380
 agtaatgaag aagattctgc ttctgtttt tcaccatcat ttggtctgaa acagacagat 4440
 aaagttccaa gtaaaacgggt agctgctaaa aagggaac cgtcttcaga tacagtccct 4500
 aagcccaaga gagcccaaaa acagaagaaa gtagtagagg ctgtaaacctc tgactcggat 4560
 tcagaatttg gcattccaaa gaagactaca acacaaaaag gtaaggccg aggggcaag 4620

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aaaaggaaag catctggctc tgaaaatgaa ggcgattata accctggcag gaaaacatcc 4680
aaaacaacaa gcaagaaacc gaagaagaca tcttttgatc aggattcaga tgtggacatc 4740
ttcccctcag acttccctac tgagccacct tctctgccac gaaccggctc g gctaggaaa 4800
gaagtataat attttacaga gtctgatgaa gaagaagatg atgttgattt tgcaatgttt 4860
aattaa 4866

<210> 84

<211> 311

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(311)

<223> 3' terminal sequence. caspase 4,
apoptosis-related cysteine protease (CASP4) gene.

<400> 84

cacttttatt gaaatacaaa atgttaaata tgcaagctgt actaatgaag gtgctccttg 60
aagttgatta aggagggctg ggctgcttgt ggcttccatt ttcaattgcc aggaaagagg 120
tagaaatata ttgtcatgga cagtgttct atgggtggca tttagacttt ggcccttgga 180
gtttcaaatg attgctgtac ctccgaaat acttctcta ggtggcagca ccaagaatat 240
ttctgggaag catgtgatga gttgtgtgat gaagatagag cccattgtg ctgtctctcc 300
cagggcacgt t 311

<210> 85

<211> 1291

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1291)

<223> caspase 4, apoptosis-related cysteine
protease (CASP4) gene.

<400> 85

gctctttcca acgctgtaaa aaaggacaga ggctgttccc tatggcagaa ggcaaccaca 60
gaaaaaagcc acttaagggtg ttggaatccc tgggcaaaga ttctctcact ggtgttttgg 120
ataacttggt ggaacaaaat gtactgaact ggaaggaaga ggaaaaaag aa atattacg 180
atgctaaaac tgaagacaaa gttcgggtca tggcagactc tatgcaagag aagcaacgta 240
tggcaggaca aatgcttctt caaacctttt ttaacataga ccaaatatcc cccaataaaa 300
aagctcatcc gaatatggag gctggaccac ctgagtcagg agaactaca gatgccctca 360
agctttgtcc tcatgaagaa ttctgagac tatgtaaaga aagagctgaa gagatctatc 420
caataaagga gagaaacaac cgcacacgcc tggctctcat catatgcaat acagagtgtg 480
accatctgcc tccgaggaat ggagctgact ttgacatcac agggatgaag gagctacttg 540
aggtctgga ctatagtgtg gatgtagaag agaactgac agccagggat atggagtcag 600
cgctgagggc atttgcctac agaccagagc acaagtcctc tgacagcaca ttcttggtac 660
tcatgtctca tggcatcctg gagggaaatct gcggaactgt gcatgatgag aaaaaaccag 720
atgtgctgct ttatgacacc atcttccaga tattcaacaa ccgcaactgc ctgagcttga 780
aggacaaacc caagtcacat attgtccagg cctgcagagg tgcaaacctg ggggaactgt 840
gggtcagaga ctctccagca tccttggaag tggcctcttc acagtcactt gagaacctgg 900
aggaagatgc tgtttacaag acccacgtgg agaaggactt cattgctttc tgctcttcaa 960

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```
cgccacacaa cgtgtcctgg agagacagca caatgggctc tatcttcac acacaactca 1020
tcacatgctt ccagaaatat tcttggtg ct gccacctaga ggaagtattt cggaaggtag 1080
agcaatcatt tgaaactcca agggccaaag ctcaaatgcc caccatagaa cgactgtcca 1140
tgacaagata tttctacctc tttcctggca attgaaaatg gaagccacaa gcagcccagc 1200
cctccttaat caacttcaag gagcaccttc attagtacag ctgcatatt taacattttg 1260
tatttcaata aaagtgaaga caaaaaaaaaa a 1291
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<210> 86

<211> 319

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(319)

<223> 5' terminal sequence. tiss ue inhibitor of
metalloproteinase 2 (TIMP2) gene.

<400> 86

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tggacccatg ggatgagtgt tttattcatg ctgtttccag gaagggatgt cagagctgga 60
ccagtcgaaa cccttggagg ctttttttgc agttggccac aggggctgtg gaggcctgct 120
tatgggtcct cgatgtcgag aaactcctgc ttgnggaen ccgcg ccgcg tnnccacgca 180
caggagccnt cacttctctt gatgcaggcg aagaacttgg cctggnnccc gttnatgttc 240
ttctctgtga cccagtcctt ccagaggcac tcgtccgggg agganatgta gcacgggatc 300
atngggcanc gcgtgatct 319
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<210> 87

<211> 1075

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1075)

<223> tissue inhibitor of metalloproteinase 2
(TIMP2) gene.

<400> 87

```
cgagcaaac acatccgtag aaggcagcgc ggccgcga g agccgcagcg ccgctcgccc 60
gccgcccccc accccgccgc cccgccgggc gaattgcgcc ccgcgcccct cccctcgcg 120
ccccgagaca aaggagagag aaagtgttgc cgccgcagcg gggcaggtga ggagggtag 180
ccgcgcggga ggggcccgcc tcggccccgg ctcagccccc gccgcgccc ccagcccgcc 240
gccgcgagca gcgcccgg ac cccccagcgg cggccccgc ccgcccagcc ccccgcccc 300
ccatggcgcg cgcggcccgc accctgcggc tggcgctcgg cctcctgctg ctggcgacgc 360
tgcttcgccc ggccgacgcc tgcagctgct ccccggtgca cccgcaacag gcgttttgca 420
atgcagatgt agtgatcagg gccaaagcgg tcagtgcgaa ggaagtggac tctggaaacg 480
acatttatgg caaccctatc aagaggatcc agtatgagat caagcagata aagatgttca 540
aagggcctga gaagatata gagtttatct acacggcccc ctcctcgcca gtgtgtgggg 600
tctcgtgga cgttgaggga aagaaggaat atctcattgc aggaaggcc gagggggacg 660
gcaagatgca catcacctc tgtgacttca tcgtgccc tg ggacaccctg agcaccacc 720
agaagaagag cctgaaccac aggtaccaga tgggctgcga gtgcaagatc acgcgctgcc 780
ccatgatccc gtgctacatc tcctccccgg acgagtgcct ctggatggac tgggtcacag 840
agaagaacat caacgggcac caggccaagt tcttcgcctg catcaagaga agtgacggct 900
```

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cctgtgcgtg gtaccgcggc gcggcgcccc ccaagcagga gtttctcgac atcgaggacc 960
cataagcagg cctccaacgc ccctgtggcc aactgcaaaa aaagcctcca agggtttcga 1020
ctgggtccagc tctgacatcc cttcctggaa acagcatgaa taaaacactc atccc 1075

<210> 88
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(225)
<223> 3' terminal sequence. d-dopachrome
tautomerase (DDT) gene.

<400> 88
ttttttgaat gaggaagctc ttttcattta ttcanatga ggatgaagaa gaggattatg 60
tgancacagg aatnttgcac gcgggataat ccaaagctgg ttatctccag gncctcantn 120
tgccaagaga tctctctgga agaagcagcc agttcacaga tgccctggat ccctccgtgc 180
ccaatcataa aaaagtcacg accgtcccta tnttgccaat ntgcc 225

<210> 89
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(312)
<223> 5' terminal sequence. d-dopachrome
tautomerase (DDT) gene.

<400> 89
cgttcctgga gctggacacg aatttgcccg ccaaccgagt gcccgcggn tngagaaac 60
gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg aacgtgacgg 120
tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg cagtgttcca 180
tctcctocat cggcgtagtg gggcaccgag agggacaacc gcagccacag cgccatttc 240
ttttgagttt tttcaccaag gagctaagcc cctgccaggg acccgat ant tattccttt 300
ttttcccttt gg 312

<210> 90
<211> 666
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(666)
<223> d-dopachrome tautomerase (DDT) gene.

<400> 90

```
gatccccggtg ccaggggaccc tgcccagttc caggcgctgc ctaaccacaga aacgactggg 60
cgccgcgtcc tggaaaggcc ccagcgcacg gacatctgag gagctgtttc cgttcctctg 120
cccgccatgc cgttcctgga gctggacacg aatttgccc ccaaccgagt gcccgcgggg 180
ctggagaaac gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgcgtg 240
aacgtgacgg tacggccggg cctggcoatg gcgctgagcg ggtccaccga gccctgcgcg 300
cagctgtcca tctcctccat cggcgtagtg ggaccgcgg aggacaaccg cagccacagc 360
gcccaattct ttgagtttct caccaaggag ctagccctgg gcc aggaccg gatacttata 420
cgctttttcc ccttgagtc ctggcagatt ggcaagatag ggacggcat gactttttta 480
tgattgggca cggagggatc cagggcattc gtgaactggc tgcttcttcc agagagatct 540
cttggcagag tgagggcctg gagataacca gctttggatt atcccgcatt caacattcct 600
gtgatcacat aatcctcttc ttcctctca tatgaaataa atgaagagag cttcctcatt 660
caaaaa
```

666

<210> 91

<211> 443

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(443)

<223> 3' terminal sequence. prolactin (PRL) gene.

<400> 91

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gantttgatg tctctaagga gtcagttttt attttttaag aggagacctg ttacacccaa 60
gcatggattc aaaagagata caactaaaag aagcttgcaa tggaaaggat cattaaggac 120
cttctcagaa atagatgaaa tggatgtggg cttagca gtt gttgttgtgg atgattcggg 180
cacttcaggg agcttgagga taattgtoga ttttatgtga atccctgcgt aggcaatggg 240
agagggtata ataaggcagg aaagggcgag actcttcata agccatctgc aggggatggg 300
aagtccccga ccagacagag gtagatctca tttcttttgg gttttcaggg atgaacctgg 360
gcttgactat ccagcttcca tgnccctctt ggaagccctt ttggttttgc tccctcaatc 420
ttctacagct tttgggttag ggt
```

443

<210> 92

<211> 243

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(243)

<223> 5' terminal sequence. prolactin (PRL) gene.

<400> 92

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gaagaatcgg aacatacagg ctttgatata aaaggtttat aaagccaata tctgggaaag 60
agaaaaccgt gagacttcca gatcttctct ggtgaagtgt gtttcctgca acgatcacga 120
acatgaacat caaaggatcg ccatgggaaa gggccctcc tgctgctgct ggggtgttcaa 180
acctgctcct gtgccagagc gtgggcccc ttggcccatc tgtcccgnc gggcttgccc 240
gat
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243

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<210> 93
<211> 833
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(833)
<223> prolactin (PRL) gene.

<400> 93
aaacatgaac atcaaaggat cgccatggaa agggtccttc ctgctgctgc tgggtgtcaaa 60
cctgctgctg tgccagagcg tggcccccctt gcccatctgt cccggcgggg ctgcccgatg 12 0
ccagggtgacc cttcgagacc tgtttgaccg cgccgtcgtc ctgtccact acatccataa 180
cctctctca gaaatgttca gcgaattcga taaacgggtat acccatggcc ggggggttcat 240
taccaaggcc atcaacagct gccacacttc ttcccttgcc acccccgaag acaaggagca 300
agcccaacag atgaatcaaa aagactttct gagcctgata gtcagcatat tgcgacccg 360
gaatgagcct ctgtatcatc tggtcacgga agtacgtggt atgcaagaag ccccgagggc 420
tattctatcc aaagctgtag agattgagga gcaaaccaaa cggcttctag agggcatgga 480
gctgatagtc agccagggtc atcctgaaac caaagaaaat gagatctacc ctgtctggtc 540
gggacttcca tccctgcag a tggctgatga agagtctcgc ctttctgctt attataacct 600
gctccactgc ctacgcaggg attcacataa aatcgacaat tatctcaagc tctgaagtg 660
ccgaatcatc cacaacaaca actgctaagc ccacatccat ttcattctatt tctgagaagg 720
tccttaataa tccgttccat tgcaagcttc ttttagttgt atctcttttg aatccatgct 780
tgggtgtaac aggtctcctc ttaaaaaata aaaactgact cgtagagac atc 833

<210> 94
<211> 304
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(304)
<223> 3' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 94
actaagcagt gtgcttttat ttcatgaac acatagtttt ataactaaca gcaaaaagta 60
aatctacaaa tcacagttag gaaacataat gatttgttct ggaatcagct gctggagaaa 120
gaggcaagtg gttaaaaatg gagcatgaaa ggagctggga gctttagtag tgtcagtcctg 180
actacattct tgaggcattt cacgtactct gtagtgttac ctgaagaaaa atcacatttt 240
aaccaatcat tccattagtc aagctatcag tgaaaggagt gtgtaaaaca tgcgggatcc 300
cggg 304

<210> 95
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. prolactin receptor
(PRLR) gene.

<400> 95
gaggtcattg agaagccaga gaatcctgaa acanccacaca cctggaaccc ccantgcata 60
agcatggaag gcaaaatccc ctatttncat gctggtggat ccaaagtgtc aacatggccc 120
ttaccacagc ccagccagca caacccagca tcctcttacc acaatattac tgatgtgtgt 180
gagctggctg tgggccctgc aggtgcaccg gccactctgt tgaatgaagc aggtaaagat 240
gctttaaaat cctctcaaac cattaagtct agagangag g gnaaggcaac ccaggcagag 300
ggaggtagga aagcttccat tcttgagnac tgaccagggg tacgncctgg gttgcttgcc 360
ccaggg 366

<210> 96
<211> 2723
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2723)
<223> prolactin receptor (PRLR) gene.

<400> 96
ggaggctgaa atcccacagac gccggttttc tgggctgggc tttctgctta ctcaactcctt 60
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atgtcctcgt gcaggaagta ctcatcgact gatgtggcag actttgctcc ctgacaaaac 180
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gtgaacttct gatacatttc ctgcagcaag agaaggcagc caacatgaag gaaaatgtgg 300
catctgcaac cgttttcaact ctgctacttt ttctcaac ac ctgccttctg aatggacagt 360
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gctggtggag gcctgggaca gatggaggac ttctaccaa ttattcactg acttaccaca 480
gggaaggaga gacactcatg catgaatgtc cagactacat aaccgggtggc cccaactcct 540
gccactttgg caagcagtac acctccatgt ggaggacata catcatgatg gtcaatgcca 600
ctaaccagat gggaagcagt ttctcggatg aactttatgt ggacgtgact tacatagtgc 660
agccagaccc tcctttggag ctggctgtgg aagtaaaaca gccagaagac agaaaaccct 720
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ccttgagta tgtggagatt cacaaggtca acaaagatgg tgcattatca ttgctacca 186 0

65/292

```
aacagagaga gaacagcggc aagcccaaga agcccgaggac tcctgagaac aataaggagt 1920
atgccaaagg gtccgggggtc atggataaca acatcctggg gttgggtgcc gatccacatg 1980
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```

<210> 97

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 97

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ttttctttta ataatgtat ttcaacgaaa atgaactgac ttaaagaaaa aatattaagg 120
aaataatcac aaagatggta cacacggatc attaaaagat acggatgtat aggatacata 180
tgtcacaaat gattaaggac ttaaaaaatg taaccctccc aagaagtggg gagcctccca 240
aagtggggga agggcaaata caatttcnt ttgggggggg ataggngac cccctttgca 300
gagagggggt aggtgggggt tcccccggn acacacaggc aagggtttgg gngccccttg 360
tgggg                                           365
```

<210> 98

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(366)

<223> 5' terminal sequence. interleukin 2
receptor, beta (IL2RB) gene.

<400> 98

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gacaaggctc cacaagcgtt gagccttgga aaggtagaca agcgttg agc cactaagcag 240
aggaccttgg gttcccaata caaaaatacc tactgctgag agggngtgct gaccattttg 300
```

gtcaaggatt tcngtttgcc ttatatccca aataaantcc ctttttttn aggtttntt 360
agtntt 366

<210> 99

<211> 4034

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4034)

<223> interleukin 2 receptor, beta (IL2RB) gene.

<400> 99

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cttcttgcca agtccatgcc tggccggaca gacggcgggt gaaccaaacc tgtgagctgc 360
tcccctggag tcaagcatcc tgggcctgca acctgatcct cggagcccca gattctcaga 420
aactgaccac agttgacatc gtcaccctga ggggtgctgt ccgtgagggg gtgcgatgga 480
gggtgatggc catcaggac ttcaagccct ttgagaacct tcgctgatg gccccatct 540
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cctccacta ctttgaaga cacctggagt tcgaggcccg gacgctgtcc ccaggccaca 660
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67/292

```

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ggggtttggc acc aagctct gtccaatcag gtaggctggg cctgaactag ccaatcagat 3360
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atctttgtta ctctgtaaat gaaaaaacc attttcgcta taaataaaag gtaactgtac 4020
aaaataagta caat
4034

```

<210> 100

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(444)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 100

```

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aactggcagt ttgtccattt gaatatcaga cctagtttct tcttaatttc cacacta ttt 120
ctcccatatt ccttaaaactt cttggcatcc ttcattgcctt acagctaccc agatgcaata 180
aagtcattgt acagtatttc ttacaatata agttatatgg caatgttcag gcattttttt 240
ttttcacagg cactaggagg accctgttta aatgggggat atgaggtcag gaatgggctt 300
attcacagga tgggggggtcc cggattcagg tgggt tgggg ancacaggac accacagggtg 360
aggctccctt tgccaaagggt ggggccaaac ataatttttg cttttctggc ctttcaaaaa 420
catatttccn tcgcgttttg gggg
444

```

<210> 101

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

68/292

<221> misc_feature
<222> (1)..(396)
<223> 5' terminal sequence. gata-binding protein 3
(GATA3) gene.

<400> 101
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acccttgact atgaagaagg aagcctatcc a gaccagaaac cgaaaaatgt ctagcaaadc 120
caaaaagtgc aaaaagtgc tgactcactg gaggacttcc ccaagaacag ctggtttaac 180
ccggccgccc tctccagaca catgtcctcc ctgagccaca tctcgccctt cagccactcc 240
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ccacaccacc cctccagctg ggtcaccgcc ntgggtttag agccttgtn gatggttcac 360
agggggcccc cagcgagagt tncctgnagt tccttt 396

<210> 102
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. placental growth
factor, vascular endothelial growth factor -related
protein (PGF) gene.

<400> 102
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acagactgcc acctgtgcgg cgatgctgtt ccccgagta acccaccct tggaggagag 120
agaccccgca cccggctcgt gtatttatta ccgtcacact cttcagtgc tctgctggt 180
acctgcctc tatttattag ccaactgtt ccctgctgaa tgctcgtc cttcaagac 240
gaggggcagg gaaggacagg accctcagga attcagtgc ttcaacaacg tga gagaaag 300
agagaagcca gccacagacc cctggggagc ttccgcttt tgaaagaagc aagacaagt 360
ggccttggt aggggcaagg ttagggccca ggaggccctn gggaagttt tcaggg 416

<210> 103
<211> 1645
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1645)
<223> placental growth factor, vascular
endothelial growth factor -related protein (PGF)
gene.

<400> 103
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tccccgggac ccgctgccc ctccgccc cgccccgcg ggccgctccc cgtcgggttc 120
cccagccaca gccttaccta cgggctcctg actccgcaag gcttcagaa gatgctcga 180
ccaccggccg gggcctcggg gcagcagtga gggaggcgtc cagccccca ctcagctctt 240
ctctcctgt gccaggggct ccccggggga tgagcatggt ggttttcct cggagcccc 300

69/292

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ataaagtatt ctagtgtgga aacgc 1645
```

<210> 104

<211> 309

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(309)

<223> 5' terminal sequence. ubiquitin protein
ligase e3a (human papilloma virus e6 -associated
protein, angelman syndrome) (UBE3A) gene.

<400> 104

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ttcgtatgga taataatgca gc agctatta aagccctcga gctttataag antagggcaa 120
aactctgtga tcctcatccc tccaagaaag gagcaagctc agcttacctt gagaactcga 180
aaggtgcccc caacaactcc tgctctgaga taaaaatgaa caaggaaagg gcgctaggaa 240
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tctttggac 309
```

<210> 105

<211> 2628

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2628)

<223> ubiquitin protein ligase e3a (human

papilloma virus e6 -associated protein, angelman
syndrome) (UBE3A) gene.

<400> 105

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ccatatttga gactcaaagt tagacgtgac catatcatag atgatgcact tgtccggcta 1620
gagatgatcg ctatggaaaa tctgcagac ttgaagaagc agttgtatgt ggaatttgaa 1680
ggagaacaag gaggatgatg gggaggtgtt tccaaagaat tttttcagct ggttgtggag 1740
gaaatcttca atccagatat tggatgttcc acatacagat aatctacaaa attgttttgg 1800
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ctggctatctt acaataactg tatactggat gtacattttc ccatggttgt ctacaggaag 1920
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cagatatcac agacagatct ttttgtaac ccaatgatgt atg atctaaa ggaaaatggt 2100
gataaaattc caattacaaa tgaaaacagg aaggaaattg tcaatcttta ttctgactac 2160
attctcaata aatcagtaga aaaacagttc aaggcttttc ggagaggttt tcatatgggtg 2220
accaatgaat ctcccttaaa gtacttattc agaccagaag aaattgaatt gottatatgt 2280
ggaagccgga atctagat tt ccaagcacta gaagaacta cagaatatga cggtggctat 2340
accagggact ctgttctgat tagggagtcc tgggaaatcg ttcattcatt tacagatgaa 2400
cagaaaagac tcttcttgca gtttacaacg ggcacagaca gagcacctgt gggaggacta 2460
ggaaaattaa agatgattat agccaaaaat ggcccagaca cagaaagggt acctaca tct 2520
catacttgct ttaatgtgct tttacttccg gaataactca gcaaagaaaa acttaaagag 2580
agattgttga aggccatcac gtatgccaaa ggatttggca tgctgtaa 2628
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<210> 106

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 106
aattttaatt ctacgacctg aagctataca agggatgct ctataaactt catgggactg 60
tcgtacacac ttgataaagt gacaactgtg caataccact tagcatctca aaatcag gaa 120
catactattg aattgcttaa acacaatcca caganttaaa aacaaaatca ggatgccatc 180
cacagttata ctaattatcc attaaaaggc ttacacttaa tacttgaant aacaatcaat 240
atctagnccg ggnatactgg aaagtggatt tcagnggtct catcctgttg gtactctatt 300
ggggnggggt ttcttgagggt aggttatggg ggact gggnc caaggntggg ggggtaccacc 360
cag 363

<210> 107

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(408)

<223> 5' terminal sequence. oncogene tc21 (TC21)
gene.

<400> 107
gaattgaatc taaaaaagtg aaccatctca gacctttact gatactacaa cttttgtttt 60
ctgatggcca aaataccaaa tgctgttgtt atttatggat taaaaactgc ttataaaacc 120
ctgtgttact actcctaactc ttggagatga taatatct ta tgtgggtcaaa tatttggact 180
catttaggac ttagataattt cagtgtactt gattttttta tttaactctt ttccacagcc 240
acgctaaggg taaaaaggaa taatttcctt ctgtcttcct tttcaagtat ttctgggtaa 300
gggattcaaa aaactaaaaac tgtttttggt tgtaatatata aatatgggat tgatctttcc 360
ggggtcagag atgattaatg tttttgctat atacttttat acatgnnt 408

<210> 108

<211> 612

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(612)

<223> oncogene tc21 (TC21) gene.

<400> 108
atggccgcgg cggctggcgg acggctccgg caggagaagt accggctcgt ggtggtcggc 60
gggggcggcg tgggcaagtc ggcgctcacc atccagttca tccagtccta ttttgtaacg 120
gattatgac caaccattga agattcttac acaagcaggt gtgtgataga tgacagagca 180
gcccggttag atattttgga tacagcagga caagaagagt t tggagccat gagagaacag 240
tatatgagga ctggcgaagg cttcctgttg gtcttttcag tcacagatag aggcagtttt 300
gaagaaaatc ataagtttca aagacagatt ctcagagtaa aggatcgtga tgagttccca 360
atgattttta ttggaataa agcagatctg gatcatcaaa gacaggtaac acaggaagaa 420
ggacaacagt tagcacggca gcttaaggta acatacatgg aggcacagc aaagattagg 480
atgaatgtag atcaagcttt ccatgaactt gtccgggtta tcaggaaatt tcaagagcag 540
gaatgtcctc cttcaccaga accaacacgg aaagaaaaag acaagaaagg ctgccattgt 600

gtcattttct ag

6 12

<210> 109
<211> 592
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(592)
<223> 5' terminal sequence. tyrosine kinase with
immunoglobulin and epidermal growth facto r
homology domains (TIE) gene.

<400> 109
ngtcggagag aacctagcct ccaagattgc agacttcggc ctttctcggg gagaggaggt 60
ttatgtgaag aagacgatgg ggcgtctccc tgtgcgctgg atggccattg agtccctgaa 120
ctacagtgtc tataccacca agagtgatgt ctggctcttt ggagtccttc tttgggagat 1 80
agtgaagcctt ggaggtagac cctactgtgg catgacctgt gccgagctct atgaaaagct 240
gccccagggc taccgcatgg agcagcctcg aaactgtgac gatgaagtgt acgagctgat 300
gcgttcagtg ctggcgggac cgtccctatg agcgaccccc ctttgcccag attgcgctaa 360
cagctaggcc gcatgctggg aagccaggga aggcctatgt gaacatgttc gctgtttgag 420
aacttcaatt aacgcgggca ttgatgccac agctgaggag gnetgagctg ccattccagcc 480
agaactnggt ctgttgccg gagcaaattt ggtgtctaaa ctgtgaccag ttnaacctta 540
aagctttgat ttaagttgct taaggatttt ttaattaag ggagaaaaat tt 592

<210> 110
<211> 3845
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3845)
<223> tyrosine kinase with immunoglobulin and
epidermal growth factor homology domains (TIE)
gene.

<400> 110
cgctcgtcct ggctggcctg ggtcggcctc tggagtatgg tctggcgggt gccccctttc 60
ttgctcccca tcctcttctt ggcttctcat gtgggcgcgg cgggtggacct gacgctgctg 120
gccaacctgc ggctcacgga cccccagcgc ttcttctga cttgcgtgtc tggggaggcc 180
ggggcgggga ggggctcgga cgcctggggc cc gccccctgc tgctggagaa ggacgaccgt 240
atcgtgcgca cccgcgccgg gccaccctcg cgcctggcgc gcaacgggtc gcaccaggtc 300
acgcttcgcg gcttctccaa gccctcggac ctcgtgggcg tcttctcctg cgtgggcgggt 360
gctggggcgc ggcgcacgcg cgtcatctac gtgcacaaca gccctggagc ccacctgctt 420
ccagacaagg tcacacacac tgtgaacaaa ggtgacaccg ctgtactttc tgcacgtgtg 480
caaaaggaga agcagacaga cgtgatctgg aagagcaacg gatactactt ctacaccctg 540
gactggcatg aagcccagga tgggcgggtc ctgctgcagc tcccaaattg gcagccacca 600
tcgagcggca tctacagtgc cacttacctg gaagccagcc cctggggcag cg ccttcttt 660
cggctcatcg tgcggggttg tgggctggg cgcctggggc caggctgtac caaggagtgc 720
ccaggttgcc tacatggagg tgtctgccac gaccatgacg gcgaatgtgt atgccccct 780
ggcttcactg gcacccgctg tgaacaggcc tgcagagagg gccgttttgg gcagagctgc 840

73/292

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caggagcagt gccaggcat atcaggctgc cggggcctca ccttctgcct cccagacccc 900
tatggctgct cttgtggatc tggctggaga ggaagccagt gccagaagc ttgtgcccct 960
ggtcattttg gggctgattg ccgactccag tgccagtgtc agaatggtgg cacttgtgac 1020
cggttcagtg gttgtgtctg cccctctggg tggcatggag tgcactgtga gaagtcagac 1080
cggatccccc agatcctcaa catggcctca gaactggagt tcaacttaga gacgatgccc 1140
cggatcaact gtgcagctgc agggaacccc ttccccgtgc ggggcagcat agagctacgc 1200
aagccagacg gcactgtgct cctgtccacc aaggccattg tggagccaga gaagaccaca 1260
gctgagttcg aggtgccccg cttggttctt gcggacagtg ggttct ggga gtgccgtgtg 1320
tccacatctg cgggccaaga cagccggcgc ttcaaggtca atgtgaaagt gcccccgctg 1380
ccccgtgctg cacctcggct cctgaccaag cagagccgcc agcttgtggt ctccccgctg 1440
gtctcgttct ctggggatgg acccatctcc actgtccgcc tgcactaccg gccccaggac 1500
agtaccatgg actggtcgac cattgtggtg gacccagtg agaactgtac gttaatgaac 1560
ctgaggccaa agacaggata cagtgttctg gtgcagctga gccggccagg ggaaggagga 1620
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gaagttctgt gcaaattggg gcatcaccac aacatcatca acctcctggg ggctgtgaag 2760
aaccgaggtt acttgtatat cgtattgaa tatgccccct acgggaacct gctagatttt 2 820
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gagaacctag cctccaagat tgcagacttc ggctt tctc ggggagagga ggtttatgtg 3060
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cagctactcc cactcccggc ctgtcattca gaaaaaata aatgttctaa taagctccaa 3840
aaaaa 384 5

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<210> 111

<211> 202

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(202)
<223> 3' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 111
aaagcccttc aaggtttact cncanctt gcaaggccca cancttggtc aaggaccaa 60
cccacaggct tttagctact ctaatttact tcaccaatga atgaaaacca taaaccaaag 120
cttgctgcct aaccactccc cagggccaga cgggacaagg aaatgctgag aggggagggg 180
acccatgggg canantnatg ag 202

<210> 112
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(450)
<223> 5' terminal sequence. autocrine motility
factor receptor (AMFR) gene.

<400> 112
attcaagtac cttttcctac acagcgggtca gatagcatca gacctgcatt gaacagtcct 60
gtggaaggc caagcagtga ccaggaagag ggagaaactt ctgctcagac cgagcgtgtg 120
ccactggacc tcagtcctcg cctggaggag acgctggact tggcgagggt ggaagtggag 180
cccagtgagg tggaagactt cgaggctcgt gggagcgtt tctccaagtc tgctgatgag 240
agacagcgca tgtggtngca gcgtaaggac gaactcctcc agcaagctcg caaacgtttt 300
cttgaacaaa agttctgaag atgatgccgg ccttcagaga gctttcctnc ccttcggaaa 360
ggtgccgttc ctttgaacc cgtgaaccc ctgncgttcg aaaggattgc ttggccttgc 420
cgccgcggga aacggaggct ttcagaagca 450

<210> 113
<211> 1810
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1810)
<223> autocrine motility factor receptor (AMFR)
gene.

<400> 113
ggggggaagg ccaagcagtg accaggaaga gggagaaact tctgctcaga ccgagcgtgt 60
gccactggac ctcatcctc gcctggagga gacgctggac ttcggcgagg tggaagtgga 120
gcccagtgag gtggaagact tcgaggctcg tgggagcgc tctccaagt ctgctgatga 180
gagacagcgc atgctggctg cagcgtaagg acgaactcct ccagcaagct cgcaaactgt 240
tcttgaacaa aagtcttgaa gatgatgcgg cctcagagag cttcctcccc tcggaagggtg 300
cgtcctctga ccccgtagc ctgcgtcgaa ggatgctggc tgccgcgcgg aacggaggct 360
tcagaagcag cagacctcct agcgctccct tgccttctc agctgcct cc tgcgcctgt 420
gcccagactga ctggaggagg cctgtcccaa ttctgccgt ccatggaaaa gcgggcttga 480

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ctgcattgcc gctgtataaa gcatgtggtc ttatagtgtt tggacagctg ataaatttaa 540
tccttccttg taatactttc tatgtgacat ttctcttccc cttagaaaca ctgcaaattt 600
taactgtagg tatgatctct tctggg gttg actggactgc ttgggggtgg ggacgatcag 660
gaggaagtga gccagtcgcc tgcctgcagc aggcagcttc tactcctgcc tcatgcatac 720
gtcccacaaa tgcaggtgtc ctgagcacca caccagtggt gaagagtgtg ggggaggcgc 780
acagtgtgag cccgccccca cgtcgtgggg taacatctgt tatcaaactg ctgtcgttgt 840
tgtggaagca tgtagactgt gccagagcca gaccacggg ctcatgcacc cctgagcagc 900
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tgctaaagcc tgtgggtttg gtccttgaac aagatgtggg ccttgcaaga tgggagagta 1260
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cactgcgttt tcctagctgt gttattcctg gtttaattca gcagagaagg taagggtgta 1380
acctacctgc cttggagagg cccaggtccc aaatctcttc aaattcttca catgtttaac 1440
tttaaggatt tgaacctga agtcatagg t acagacctc agttttatgc cccattgga t 1500
tacttttttt tttttttttt tttttttact ctttgaaagc tttgttttgt ggtagtcgct 1560
tttggaaga atccagtatt atctacaatt attggcaaag tttaaagtta ttttacataa 1620
cggaaggtt ttagaagtgt gaaaagtaat tgaaaaagg gataggtaaa ttttaggca 1680
aagataattt atttcaataa atctttcaaa agc cttacct tgaaatgctg ttagtaaatt 1740
tctgtgcatt tttttttttt aatttgttt gctgagagca tagctatttg tttttattgt 1800
aaaccgccc                                     1810

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<210> 114

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(248)

<223> 3' terminal sequence. homo sapiens mrna;
 cdna dkfzp434c136 (from clone dkfzp434c136) (EST
 R81127) gene.

<400> 114

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gaaattccaa aatcactcta gttattcac ataatatagn atttgattcc attcttttgn 60
actgtncnccn acttttacaa tgtgtacaat gtttcacat gtnccaatta atgggtgagc 120
tttaaatgaa aatattctgg ancttccatt tatnggnatc aaccacaata gcaagacccc 180
cangaaatac ttgatctaaa ctgggagggt ccaacacaat tttttttttt aatgggnctt 240
gccacctt                                     248

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<210> 115

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
 (BCL2) gene.

<400> 115
ttttttaaag cagcttttga aatatcaacc acagcattaa acattgaaca gagtacattc 60
caaagttaat acagataaat ggtatataat gcaataatgc cacagagtta ttccatcaat 120
gtttcanggc tgattctaaa ctggangaaa aaaaaaattn cctagtttat ttgctganga 180
tgtcacttct tttgttactt ctttatagtt ccccaccatt gatTTTTttt ttaatgcccc 240
ggggtgtaca ggataacccc catattccac accggggnac tttttttttg tcagggtttt 300
caaataaanc caaactacag tgacaggata atgttttaca ggtaattccn tgggccgggg 360
ggtcaattat ncctggacac ctcaactcaa ggcntccttt gggggtttgg gggcc 415

<210> 116
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(468)
<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 116
aattgtgcc aaaaagcatt ttagcaattt atacaatatc atccagtacc ttaagccctg 60
attgtgtata ttcatatatt ttggatacgc accccccaac tccaataact ggctctgtct 120
gagtaagaaa cagaatcctc tggaaactga ggaagtgaac atttcggtga cttccgcac 180
aggaaggcta gagttacca gagcatcagg ccgccacaag tgctgtctt t aggagaccg 240
aagtccgcag aacctgcctn tgtcccagct tggaggcctg gtctgggaa ctgagccggg 300
gccctcactn gcctcctoca gggatgatca acaggngcag tgtggtntcc gaatgtctgg 360
aagcttgatg ggagctcaga atttccactg ttcaagaaag agncagtaga ggggtgtngc 420
tgggnctgtt cacctggggg ccctncaggt agngcccntt tttcacgt 468

<210> 117
<211> 6030
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(6030)
<223> b-cell cll/lymphoma 2 (BCL2) gene.

<400> 117
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taaccgggag atagtgatga agtacatcca ttataagctg tcgcagaggg gctacgagtg 120
ggatgcggga gatgtgggag ccgcgcccc gggggccggc ccgcgcccgg gcatcttctc 180
ctcgcagccc gggcacagc ccatacagc cgcattcccg gaccgg gtcg ccaggacctc 240
gcccgtgcag accccggctg ccccggcgcg cgccggggg cctgcgtca gcccggtgcc 300
acctgtggtc cacctgaccc tccgccaggc cggcgacgac ttctcccgcc gctaccgccc 360
cgacttcgcc gagatgtcca ggcagctgca cctgacgccc ttcaccgcgc ggggacgctt 420
tgccacggtg gtggaggagc tctt caggga cgggggtgaac tgggggagga ttgtggcctt 480
ctttgagttc ggtggggtca tgtgtgtgga gacgtcaac cgggagatgt cggccctggt 540
ggacaacatc gccctgtgga tgactgagta cctgaaccgg cacctgcaca cctggatcca 600
ggataacgga ggctgggatg ctttgtgga actgtacggc cccagcatgc ggcctctgtt 660

tgatttctcc tggctgtctc tgaagactct gctcagtttg gccctggtgg gagcttgcac 720
caccctgggt gcctatctgg gccacaagtg aagtcaacat gcctgcccc aacaaatatg 780
caaaagggtc actaaagcag tagaaataat atgcattgtc agtgatgttc catgaaacaa 840
agctgcaggc tgtttaagaa aaaataacac acatataaac atca cacaca cagacagaca 900
cacacacaca caacaattaa cagtcttcag gcaaaacgtc gaatcagcta tttactgcca 960
aagggaataa tcatttattt tttacattat taagaaaaaa agatttattt atttaagaca 1020
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<210> 118

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 5' terminal sequence. v-erb-b2 avian
erythroblastic leukemia viral oncogene homolog 2
(neuro/glioblastoma derived oncogene homolog)
(ERBB2) gene.

<400> 118

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<210> 119

<211> 4530

<212> DNA/RNA

<213> Artificial Sequence

<220>

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<220>

<221> misc_feature

<222> (1)..(4530)

<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 119

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80/292

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<210> 120
<211> 319
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(319)
<223> 5' terminal sequence. mouse double minute 2,
human homolog of; p53-binding protein (MDM2) gene.

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<210> 121
<211> 2372
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

<222> (1)..(2372)

<223> mouse double minute 2, human homolog of;
p53-binding protein (MDM2) gene.

<400> 121

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<210> 122

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(343)

<223> 3' terminal sequence. gata-binding protein 3
(GATA3) gene.

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gtaattctag gttttatttc caacccaaaa nttgaggaga gga 343

<210> 123
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(258)
<223> 3' terminal sequence. src homology 3
domain-containing protein hip -55 (HIP-55) gene.

<400> 123
cgagtgaagt atgttgagg aacatgttgt gtctgccgtt tttgaatacc cagggtgga 60
gcttgccat ctgcatcccc acttcccata gcccaggcag agggac agag aaatggagtn 120
gggagcacag agcaggctcc aacaagacaa attccctgct gccaaaccac catgatccac 180
tctgactttg gncacaaact ctgctaaaaa caattctcta cgttcactgt tcccaagggg 240
canttttaaa cagtgggtg 258

<210> 124
<211> 443
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(443)
<223> 5' terminal sequence. src homology 3
domain-containing protein hip -55 (HIP-55) gene.

<400> 124
gccagggctc agtgggcaag ggctctgtgc cgtngnccctg tacgactacc atgcagccga 60
cgacacagag atctcctttg accccgagaa cctcatcacg ggcatcgagg tgatcgacga 120
aggetggtgg cgtggctatg ggccggatca tntgttingca tgttccctgc caactacgtg 180
gagctcattg agtgaggctg agggcacatc ttgcccttcc cctctcagac atggcttc ct 240
tattgctgga agaggaggcc tggggagtgt acattcagca ctcttcagg gaatagggac 300
ccccagttga ggattgagge ntcagggttc cctccggnnt gggcagattc agccttttca 360
cccaaattg cagcaattgg cntgggtgat ttcccacaaa tcnttctctg cattcccccg 420
acctttccca gacagtttg ttt 443

<210> 125
<211> 1331
<212> DNA/RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1331)

<223> src homology 3 domain-containing protein
hip-55 (HIP-55) gene.

<400> 125

```
atggcggcga acctgagccg gaacgggcca gcgctgcaag aggcctacgt ggggtggtc 60
accgagaagt ccccgaccga ctgggtcttc ttacctatg aaggcaacag caatgacatc 120
cgcggtggctg gcacagggga ggggtggcctg gaggagatgg tggaggagct caacagcggg 180
aaggtgatgt acgccttctg cagagtgaag gaccccaact ctggactgcc caaatgtgtc 240
ctcatcaact ggacaggcga gggcgtgaac gatgtgcgga agggagcctg tgccagccac 300
gtcagcacca tggccagctt cctgaagggg gcccatgtga ccatcaacgc acgggcccag 360
gaggatgtgg agcctgagtg catcatggag aaggtggcca aggcctcagg tgccaactac 42 0
agctttcaca aggagagtgg ccgcttcacg gacgtgggac cccaggcccc agtgggctct 480
gtgtaccaga agaccaatgc cgtgtctgag attaaaaggg ttggtaaaga cagcttctgg 540
gccaaagcag agaaggagga ggagaaccgt cggctggagg aaaagcggcg ggccgaggag 600
gcacagcggc agctggagca ggagcgccgg gacgctgagc tgcgtgaggc tgcacgccgg 660
gagcagcgct atcaggagca ggggtggcag gccagcccc agaggacgtg ggagcagcag 720
caagaagtgg tttcaaggaa ccgaaatgag caggagtctg ccgtgcaccc gagggagatt 780
ttcaagcaga aggagagggc catgtccacc acctccatct ccagtcctca gcctggcaag 840
ctgaggagcc ccttcctgc a gaagcagctc acccaaccag agaccactt tggcagagag 900
ccagctgctg ccatctcaag gccagggca gatctccctg ctgaggagcc ggcgcccagc 960
actcctccat gtctggtgca ggcagaagag gaggtgtgt atgaggaacc tccagagcag 1020
gagaccttct acgagcagcc cccactggtg cagcagcaag gtgccggctc tgagcacatt 1080
gaccaccaca ttcagggccca ggggtcagtg gggcaagggc tctgtgcccg tgccctgtac 1140
gactaccagg cagccgacga cacagagatc tcctttgacc ccgagaacct catcacgggc 1200
atcgaggtga tcgacgaagg ctggtggcgt ggctatgggc cggatggcca ttttggcatg 1260
ttccctgcca actacgtgga gtcattgag tgag gctgag ggcggccgct agactagtct 1320
agagaaaaaa c 1331
```

<210> 126

<211> 430

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(430)

<223> 3' terminal sequence. cathepsin d (lysosomal
aspartyl protease) (CTSD) gene.

<400> 126

```
gtatttccat gtcagctggg gctctcagcc gcccaagggg aggacaacag aggtcagctg 60
cagaggaagg ctggcaccag cccaatccc aacccacact ccaggccaat acatgcccct 120
gggactggct cagtccagc accaccctgc aggtccaac aaggtgggtt ttgtcccctc 180
tactccttc cagtcattc tcaggcctct agcggcctca tcctcaacgg gcccgggaca 240
ctgaacaggt aggtgggca gagccagctg ggncccaagc tnggcaagag gggccctcag 300
gcagggcagg ttttncaagg gagggncgcc gaggacggcc ttgggtnttg g ggtaagggc 360
ttaanccagt cngggctttg gtaaggggcc ggnaagggat tcntgggna aattaaagg 420
aanccccagg 430
```

<210> 127

84/292

<211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(339)
 <223> 5' terminal sequence. cathepsin d (lysosomal
 aspartyl protease) (CTSD) gene.

<400> 127
 gtggatgagg tgcgcgactg cagaaggcca tcggggcgtn gccgctgatt cagggcgagt 60
 acatgatccc ctgtgagaag gtgtccacc c tgcccgcgat cacactgaag ctgggaggca 120
 aaggctacaa gctgtcccca gaggactaca cgctcaaggt gtcgcaggcc gggaagaccc 180
 tctgcctgag cggttcatg ggcatggaca tcccgccacc cagcggncac tctggatcct 240
 ggggcgacgt cttcattcgg ccgttantac attgtgtttt gaccgtgaca acaacagggt 300
 tgggtttcgc gaggcttgcc cgcttttagt ttcccaagg 339

<210> 128
 <211> 1988
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1988)
 <223> cathepsin d (lysosomal aspartyl protease)
 (CTSD) gene.

<400> 128
 ccatgcagcc ctccagcett ctgccgctcg cctctgcct gctggctgca cccgcctcgg 60
 cgctcgtcag gatcccgctg cacaagttca cgctccatccg ccggaccatg tcggagggtg 120
 ggggctctgt ggaggacctg attgccaaag gcccgcgtctc aaagtactcc caggcgggtg 180
 cagccgtgac cgagggggccc attcccaggg tgctcaagaa ctacatggac gccagttact 240
 acggggagat tggcatcggg acgccccccc agtgcctcac agtcgtcttc gacacgggct 300
 cctccaacct gtgggtcccc tccatccact gcaaactgct ggacatcgct tgctggatcc 360
 accacaagta caacagcgac aagtccagca cctacgttaa gaatggtacc tcgtttgaca 420
 tccactatgg ctccggcagc ctctccgggt acctgagcca ggacactgtg tcggtgccct 480
 gccagtcagc gtcgtcagcc tctgccctgg gcggtgtcaa agtggagagg caggtctttg 540
 gggaggccac caagcagcca ggcatacct tcatcgagc caagttcgat ggcatacctg 600
 gcatggccta ccccgcatc tccgtcaaca acgtgctgcc cgtcttcgac aacctgatgc 660
 agcagaagct ggtggaccag aacatcttct ccttctacct gagcagggac ccagatgcgc 720
 agcctggggg tgagctgatg ctgggtggca cagactccaa gtattacaag ggttctctgt 780
 cctacctgaa tgtacccgc aaggcctact ggcaggtcca cctggaccag gtggagggtg 840
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 tgattcaggg cgagtacatg atcccctgtg agaaggtgtc caccctgccc gcgatcacac 1020
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 ccagcacaga aa cagaggag agtcccagag caggaggccc ctggcccagc ggcccctccc 1320
 acacacaccc acacactcgc ccgcccactg tcctgggcgc cctggaagcc ggccggccaa 1380
 gcccgacttg ctgttttgtt ctgtggtttt cccctccctg ggttcagaaa tgctgcctgc 1440

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ctgtctgtct ctccatctgt ttggtggggg tagagctgat ccagagcaca g atctgtttc 1500
gtgcattgga agaccccacc caagcttggc agccgagctc gtgtatcctg gggctccctt 1560
catctccagg gagtcccctc cccggcccta ccagcgcccg ctggctgagc cctacccca 1620
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gatgaggccg cttagaggct gaggatgagc tggaaggagt gagaggggac aaaaccacc 1800
ttgttgagc ctgcagggtg gtgctgggac tgagccagtc ccaggggcat gtattggcct 1860
ggagggtggg ttgggattgg gggctgggtgc cagccttcct ctgcagctga cctctgtgt 1920
cctccccttg ggcggtgag agccccagct gacatggaaa tacagttgtt ggcctccggc 1980
ctcccctc
1988

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<210> 129

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 5' terminal sequence. insulin-like growth factor 1 receptor (IGF1R) gene.

<400> 129

```

gtggcggcac tcattgttct cgggtgcagc ccgcttccca cacgtgcttg tggcacattt 60
tctggcagcg gtttgtggtc cagcagcggg agttgtactc at tgttgatg gtggtcttct 120
cacacatcgg cttctcctcc atggtccctg gacacaggtc cccacattcc tttgggggct 180
tattccccac aatgtagtta ttggacaccg catccaggat cagggaccag tccacagtng 240
agaggttaaca gaggtcagca tttttctcaa tctgatggc ccccgagta atgttcctca 300
ggttgtaaag cccaatatcc ttgaggatgg gtcaatcttc gaaggatgaa ccaggggcnt 360
aggttntttg gaaggagntt ttcca
385

```

<210> 130

<211> 4989

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4989)

<223> insulin-like growth factor 1 receptor (IGF1R) gene.

<400> 130

```

tttttttttt ttttgagaaa gggaatttca tcccaaataa aaggaatgaa gtctggctcc 60
ggaggagggt ccccgacctc gctgtggggg ctctgtttc tctccgcgc gctctcgctc 120
tgcccgacga gtgga gaaat ctgcgggcca ggcacgaca tccgcaacga ctatcagcag 180
ctgaagcgcc tggagaactg cacggtgac gagggctacc tccacatcct gctcatctcc 240
aaggccgagg actaccgcag ctaccgcttc cccaagctca cggtcattac cgagtacttg 300
ctgctgttcc gactggctgg cctcgagagc ctcgagacc tcttcccaa cctcacg gtc 360
atccgcggct ggaaactctt ctacaactac gccctggtca tcttcgagat gaccaatctc 420
aaggatattg gcttttacia cctgaggaac attactcggg gggccatcag gattgagaaa 480
aatgctgacc tctgttacct ctccactgtg gactggtccc tgatcctgga tgcgggtgcc 540
aataactaca ttgtggggaa taagcccca aagga atgtg gggacctgtg tccagggacc 600

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atggaggaga agccgatgtg tgagaagacc accatcaaca atgagtacaa ctaccgctgc 660
 tggaccacaa accgctgccca gaaaatgtgc ccaagcacgt gtgggaagcg ggctgtgcacc 720
 gagaacaatg agtgctgccca ccccgagtgc ctgggcagct gcagcgcgcc tgacaacgac 780
 acggcctgtg tagcttgccg ccactactac tatgccggtg tctgtgtgcc tgcctgcccg 840
 cccaacacct acaggtttga gggctggcgc tgtgtggacc gtgacttctg cgccaacatc 900
 ctcagcgccg agagcagcga ctccgagggg tttgtgatcc acgacggcga gtgcatgcag 960
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 gctcctgtg aaagtgcagt cctgcatttc acctccacca ccacgtcgaa gaatcgcatc 1560
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 gccaacacca ccagtctcag ccgaagcagg aacaccacgg ccttcttttg agagcagagt ggataacaag 2340
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 gagagaactg tcattttctaa ccttcggcct ttacacattgt accgcatcga tatccacagc 2460
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 ttgatcgtg gagggttggt gattatgctg tacgtcttcc atagaaagag aaataacagc 2940
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 gtgtacgttc ctgatgagt ggaggtggct cgggagaaga tcaccatgag ccgggaactt 3060
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 acctgctgat ccttgatcc tgaatctgtg caaacagtaa cgtgtgcgca cgcgcagcgg 4200
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gactgcccct gctgtgctgc tcaaggccac aggcacacag gtctcattg c ttctgactag 4920
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tgaaccggc 4989
```

<210> 131

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> 5' terminal sequence. insulin receptor
(INSR) gene.

<400> 131

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gtatctaaaa atccgcgat cctacgctct ggtgtcactt tccttc ttcc ggaagttacg 120
tctgattcga ggagagacct tggaaattng gaactactcc ttctatgcct tggacaacca 180
gaacctaaag cagctctggg actggagcaa acacaacctc accatcactc aggggaaact 240
cttcttcac tataaccca aactctgctt gtcagaaatc cacaagatgg gaaggaggtt 300
tcagggaacc aagggnccg caggaggaga aacgacattt nccctggaag gaccaatggg 360
gggaccaggg catcctgttg aaaaatggag tttactttaa anttttgctt taacattngg 420
gacntttttt tggacaagtt tttgttgaa gttggggagc cctnattttg 470
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<210> 132

<211> 4691

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4691)

<223> insulin receptor (INSR) gene.

<400> 132

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ccagcgccgc gcgctgac cgaggagacc ccgcgctccc gcagc catgg gcaccggggg 120
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cctcacggtc atccggggat cagcactgtt ctttaactac gcgctgggtca tcttcgagat 480
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 catcgagaag aacaatgagc tctgttactt ggccactatc gactgggtccc gtatcctgga 600
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<210> 133

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. forkhead box ola
(rhabdomyosarcoma) (FOXO1A) gene.

<400> 133

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<210> 134

<211> 5723

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5723)

<223> forkhead box ola (rhabdomyosarcoma) (FOXO1A)
gene.

<400> 134

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91/292

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<210> 135

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 3' terminal sequence. epidermal growth
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viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 135

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<210> 136

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(450)

<223> 5' terminal sequence. epidermal growth
factor receptor (avian erythroblastic leukemia
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 136

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<210> 137

<211> 5532

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5532)

<223> epidermal growth factor receptor (avian
erythroblastic leukemia viral (v-erb-b) oncogene
homolog) (EGFR) gene.

<400> 137

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gctctggcca caacagggca ttttacaggt gcgaatgaca gtagcattat gagtagtgt 5100
aattcaggta gtaaatatga aactagggtt tgaaattgat aatgctttca caacatttgc 5160

94/292

```

agatgtttta gaaggaaaaa agtt ccttcc taaaataatt tctctacaat tggaagattg 5220
gaagattcag ctagttagga gccattttt tcctaattctg tgtgtgccct gtaacctgac 5280
tggttaacag cagtcctttg taaacagtgt tttaaactct cctagtcaat atccacccca 5340
tccaatttat caaggaagaa atggttcaga aaatattttc agcctacagt tatgttcagt 540 0
cacacacaca tacaaaatgt tccttttgct tttaaagtaa tttttgactc ccagatcagt 5460
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atattcattt cc 5532

```

<210> 138

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 138

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ggatnagant ttanaggcaa gacatttatt cactcatgat atatcagtc aaagtgtgcc 60
tacagtatac aaggtaaaact cacaactcat caaaactaaa actttttaca atgtgcaata 120
catgtaggga tattaattca atatataaat gtcacatgtc tcccaaattgt caccaggct 180
ttctgttatt tcttaaaata tacaagtcaa t attaccaga gaaaagataa gaaaatccca 240
ttattttatc ctaaaacttat gtatacttct ctaaagattc ttagggttg taagcaatga 300
ggtttaaggc natttttttag gatgttagca tcccggggct gacttngccg ggctgtggga 360
acccaggnc cgagtggtg 378

```

<210> 139

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. tek tyrosine kinase,
endothelial (venous malformations, multiple
cutaneous and mucosal) (TEK) gene.

<400> 139

```

gctttcactg gcatgggaga cccttgacac ctgtgagaa aacatgcctc tgccaaagga 60
tgtgatatat aagtgtacat atgtgctgta cacctgggac cttcaccact gtagatccca 120
tgcattgata tatgtagat gctctgactc taataggact gtatatactg ttttaagaat 180
gggctgaat cagaatgcct gtttgtggtt tcatatgcaa taatatattt ttttaaaaat 240
gtggacttca taggaaggcg tgagtacaat tagtataatg cataactcat tgttgccta 300
ggatatattg atatttacct ttatgttga atgtatttaa atgttttcn gtgtccaaag 360
taaaatattg ttttaataaac ctaacaatgg accocgatag tacag ggtta agtgagggga 420
accttatgga ttctaacaag tcctagg 447

```

<210> 140

<211> 4138
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4138)
<223> tek tyrosine kinase, endothelial (venous
malformations, multiple cutaneous and mucosal)
(TEK) gene.

<400> 140
cttctgtgct gttccttctt gcctctaact tgtaaacaag acgtactagg acgatgctaa 60
tggaagtca caaacgctg ggtttttgaa aggatccttg ggacctcatg cac atttgtg 120
gaaactggat ggagagattt gggaagcat ggactcttta gccagcttag ttctctgtgg 180
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cctacctctt gtatctgatg ctgaaacatc tctcacctgc attgcctctg ggtggcgccc 300
ccatgagccc atcaccatag gaagggactt t gaagcctta atgaaccagc accaggatcc 360
gctggaagtt actcaagatg tgaccagaga atgggctaaa aaagtgtgtt ggaagagaga 420
aaaggctagt aagatcaatg gtgcttattt ctgtgaaggc cgagttcgag gagaggcaat 480
caggatacga accatgaaga tgcgtcaaca agcttctctc ctaccagcta cttaactat 540
gactgtggac aagggagata acgtgaacat atctttcaaa aaggtattga ttaaagaaga 600
agatgcagtg atttcaaaaa atggttctct catccattca gtgccccggc atgaagtacc 660
tgatattcta gaagtacacc tgctcatgac tcagccccag gatgctggag tgtactcggc 720
caggtatata ggaggaacc tcttcacctc ggccttcacc aggctgatag t cggagatg 780
tgaagcccag aagtggggac ctgaatgcaa ccatctctgt actgcttgta tgaacaatgg 840
tgtctgccat gaagatactg gagaatgcat ttgcccctct gggtttatgg gaaggacgtg 900
tgagaaggct tgtgaactgc acacgttttg cagaacttgt aaagaaaggc gcagtggaca 960
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aggctggaag ggtctgcagt gcaatgaagc atgccaccct ggtttttacg ggccagattg 1080
taagcttagg tgcagctgca acaatgggga gatgtgtgat cgcttccaag gatgtctctg 1140
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gatagtggat ttgccagatc atatagaagt aaacagtggt aaatttaatc ccatttgcaa 1260
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aaacgtgatt gacactggac ataactttgc tgtcatcaac atcagctctg agccttactt 1560
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ttggcaacat attcaagt ga caaatgagat tgttacactc aactatttgg aacctcggac 1680
agaatatgaa ctctgtgtgc aactgggtccg tcgtggagag ggtggggaag ggcatcctgg 1740
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ggagggcaat tttggccaag ttcttaaggc gcgcatcaag aaggatgggt tacggatgga 2700
tgctgccatc aaaagaatga aagaatatgc ctccaaagat gatcacaggg actttgcagg 2760

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```
agaactggaa gttctttgta aacttggaca ccatccaaac atcatcaatc tcttaggagc 2820
atgtgaacat cgaggctact tgtacctggc cattgagtag ggcgcccacg gaaaccttct 2880
ggacttcctt cgcaagagcc gtgtgctgga gacggaccca gcatttgcca ttgccaata g 2940
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gcacattgta aaaagtttta gttttgatga gttgtgagtt taccttgat actgtaggca 4080
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```

<210> 141

<211> 395

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(395)

<223> 3' terminal sequence. tumor necrosis factor
receptor superfamily, member 6 (TNFRSF6) gene.

<400> 141

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taattccaaa cacaaggggc aaaaaaatcc tccataaatg gaagttcttt aggtggttcc 60
aggnatctgc ttcagtttat aa ctatcttc acagtttaca ttacagaaa tataaatatt 120
atttcttaaa attcacattt aatacaaaact ttcaaagata tttaaacgta ggatagtagt 180
aaggagaatc ttaaacttta gaaacttggg ggtatgacaa gagcaattcc taaatccaga 240
tgatgatttt accattgcta tgtataagct gccatttgta ggcaggtttt acatggggac 300
attattgaac attttcgggg ggtgggggga aaaataaggn atctatttta tccatctttg 360
gattggcaaa cctgggggtc angacatgtt caca 395
```

<210> 142

<211> 461

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(461)

<223> 5' terminal sequence. tumor necrosis factor

receptor superfamily, member 6 (TNFRSF6) gene.

<400> 142

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tcgtaattgg catcaacttc atggaaagaa agaagcgtat gacacattga ttaaagatct 60
caaaaaagcc aatcttttga ctcttcgag a gaaaattcag actatcatcc tcaaggacat 120
tactagtgcac tcagaaaatt caaacttcag aaatgaaatc caaagcttgg tctagagtga 180
aaaacaacaa attcagttct gagtatatgc aattagtgtt tgaaaagatt cttaatagct 240
ggctgtaaatt actgcttgggt tttttactgg gtacatttta tcatttatta gcgctgaaga 300
gccaacatat ttgtaggttt ttaatatctc catggattct gcctccaagg gtgtttaaaa 360
tctagttggg ggaacaaaac ttccttcaag ggttaaatgc ngtggcctgg ctaagtaccc 420
ccattaggga gtgtttgccg ggggttgnaa ggtttaggtt t 461
```

<210> 143

<211> 2551

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2551)

<223> tumor necrosis factor receptor superfamily,
member 6 (TNFRSF6) gene.

<400> 143

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gtgacttggc tggagcctca ggggcgggca ctggcacgga acacaccctg aggccagccc 120
tggtgccca ggcgagctg cctcttctcc cgcggttgg tggaccgct cagtacggag 180
ttggggaagc tctttcactt cggaggattg ctcaacaacc atgctgggca tctggaccct 240
cctacctctg gttcttacgt ctgttgct ag attatcgctc aaaagtgtta atgcccaagt 300
gactgacatc aactccaagg gattggaatt gaggaagact gttactacag ttgagactca 360
gaacttggaa ggcctgcac atgatggcca attctgccaat aagccctgtc ctccagggtga 420
aaggaaagct agggactgca cagtcaatgg ggatgaacca gactgcgtgc cctgccaaga 480
agggaggag tacacagaca aagcccattt ttcttccaaa tgcagaagat gtagattgtg 540
tgatgaagga catggcttag aagtggaaat aaactgcacc cggaccaga ataccaagt 600
cagatgtaaa ccaaactttt ttgttaactc tactgtatgt gaacactgtg acccttgcac 660
caaatgtgaa catggaatca tcaaggaatg cacactcacc agcaacac ca agtgcaaaaga 720
ggaaggatcc agatctaact tgggttggtc ttgtcttctt cttttgccaa ttccactaat 780
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gaaagaagcg tatgacacat tgattaaaga tctcaaaaaa gccaatcttt gtactcttgc 1140
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cagaaatgaa atccaaagct tgggtctagag tgaaaaacaa caaattcagt tctgagtata 1260
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acagtttatt ggtgtcatat tatacaatat ttcaattgtg aattcacata gaaaacatta 1860
aattataatg ttgactatt atatatgtgt atgcatttta ctggctcaaa actacctact 1920
tctttctcag gcatcaaaag cattttgagc aggagagtat tactagagct ttgccacctc 1980
```

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```

tccatttttg ccttggtgct catottaat g gcctaata gca ccccaaaaca tggaaatata 2040
accaaaaaat acttaatatg ccacaaaag gcaagactgc ccttagaaat tctagcctgg 2100
tttgagata ctaactgctc tcagagaaag tagctttgtg acatgtcatg aacctatgtt 2160
tgcaatcaaa gatgataaaa tagattctta tttttccccc acccccgaaa atgttcaata 2220
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ggaaccacct aaagaacttc catttatgga ggattttttt gccccttgtg tttggaatta 2520
taaaatatag gtaaaagtac gtaattaaat a 2551

```

<210> 144

<211> 434

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(434)

<223> 3' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 144

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aaagtcacta agaatcattt attnagcacc tgctgtatat tcagcattgt gggaggagct 60
gtgaaagaca cagaacagta cagggtgtgg tccctgccct cgagagggtt acagtctagg 120
tgagagaaac ggaaccagga cacatgggga gccgagagaa aacagtccag gccagtatgt 180
tacaggagct ggaaggtntt tggggtcaga cccaataact ccaagtacac taagcacttc 240
agtccttcca ggggtcaac gttagtcca ggaagacaa ctactcccag ccccatatga 300
gccacgtgg catgccctgt ccatagcctc tactgccacc atcttaaaat gtctgactcc 360
ttgttccgct ggctaattca aagtcaatg aactggggag ggatgggggt gatgaggaag 420
gttcgntgga cggt 434

```

<210> 145

<211> 257

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(257)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

<400> 145

```

cttgtgtgc ntncagggg a gcaggctgaa ggggtccccag gtggacctgg agactctcag 60
ggtcgaaaac ggcggcagac cagcatgaca gatttctacc actccaaacg ccggctgac 120
ttctccaaga ggaagcccta atccgccac aggaagcctg cagtcctgga agcgcgaggg 180
cctcaaagc cntnctnaca tcttctgcct tagtctcagt ttgtgtgtct taattattat 2 40
ttgtgtttta aattttt 257

```

<210> 146

<211> 2121

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<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2121)

<223> cyclin-dependent kinase inhibitor 1a (p21,
cip1) (CDKN1A) gene.

<400> 146

```
gccgaagtca gttccttgtg gagccggagc tgggcgcgga ttgcgcgagg caccgaggca 60
ctcagaggag gcgccatgtc agaaccggct ggggatgtcc gtcagaacct atgcggcagc 120
aaggcctgcc gcgcctctt cggcccagtg gacagcgagc agctg agccg cgactgtgat 180
gcgctaattg cgggctgcat ccaggaggcc cgtgagcgat ggaacttcga ctttgtcacc 240
gagacaccac tggagggtga cttgccttg gagcgtgtgc ggggccttgg cctgcccag 300
ctctaccttc ccacggggcc ccggcgaggc cgggatgagt tgggaggagg caggcggcct 360
ggcacctcac ctgctctgct gca ggggaca gcagaggaag accatgtgga cctgtcactg 420
tcttgtaccc ttgtgcctcg ctcaggggag caggetgaag ggtccccagg tggacctgga 480
gactctcagg gtcgaaaacg gcggcagacc agcatgacag atttctacca ctccaaacgc 540
cggctgatct tctccaagag gaagccctaa tccgcccaca ggaagcctgc agtcctgga 600
gcgcgagggc ctcaaaggcc cgctctacat cttctgcctt agtctcagtt tgtgtgtctt 660
aattattatt tgtgttttaa tttaaacacc tcctcatgta cataccctgg ccgccccctg 720
ccccccagcc tctggcatta gaattattta aacaaaaact aggcggttga atgagagggt 780
cctaagagtg ctgggcattt ttattttatg aaatactatt taa agcctcc tcatcccgtg 840
ttctcctttt cctctctccc ggaggttggg tgggcgggct tcatgccagc tacttctccc 900
tccccacttg tccgctgggt ggtacctctt ggaggggtgt ggtccttcc catcgctgtc 960
acaggcgggt atgaaattca ccccttttcc tggacactca gacctgaatt ctttttcatt 1020
tgagaagtaa acagatggca ctttgaaggg gcctcaccga gtgggggcat catcaaaaac 1080
tttgagtgcc cctcacctcc tctaagggtg gcaggggtga ccctgaagtg agcacagcct 1140
agggctgagc tggggacctg gtacctcctt ggtctttgat accccctctt gtcttgtgaa 1200
ggcaggggga aggtggggtg ctggagcaga ccaccccgcc tgcctcatg gccctctga 1260
cctgcactgg ggagcccgtc tcagtgttga gccttttccc tctttggctc ccctgtacct 1320
tttgaggagc cccagcttac ccttcttctc cagctgggct ctgcaattcc cctctgctgc 1380
tgtccctccc ccttgtcttt cccttcagta ccctctcatg ctccagggtg ctctgagggt 1440
cctgtcccac cccaccccc agctcaatgg actg gaaggg gaaggagcac acaagaagaa 1500
gggcacccca gttctacctc aggcagctca agcagcgacc gccccctct ctagctgtgg 1560
gggtgagggt cccatgtggg gccacaggcc cccttgagtg gggttatctc tgtgttaggg 1620
gtatatgatg ggggagtaga tctttctagg agggagacac tggccctca aatcgtccag 1680
cgaccttctc catcaccccc atccctcccc agttcattgc actttgatta gcagcggaac 1740
aaggagtcag acattttaag atggtggcag tagaggctat ggacagggca tgccacgtgg 1800
gctcatatgg ggctgggagt agttgtcttt cctggcacta acgttgagcc cctggaggca 1860
ctgaagtgct tagtgtactt ggagtattgg ggtctgacct caaacacc tt ccagctcctg 1920
taacatactg gcctggactg tttctctctg gctccccatg tgcctgggt cccgtttctc 1980
cacctagact gtaaacctct cgagggcagg gaccacaccc tgtactgttc tgtgtcttcc 2040
acagctcttc ccacaatgct gaatatagc cagggtgtca ataatgatt cttagtgtact 2100
ttaaaaaaaaa aaaaaaaaaa a                                     2121
```

<210> 147

<211> 452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(452)

<223> 3' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 147

```
gatttgctaa ttgcttttatt cagaagagac cccccggagt acagcttctt tggttaagca 60
cggagttgag gtggaggaga gcagtagaag gctggaaatc tgctggatgt ctcattctgg 120
gtgggtatag aagggtcctt gcctggcctc taggatgggt gagggatgct ttctgcatgg 180
ccaaggaact tggtaggggt agggagggag ggtatgagag agggaaattc agcactgggt 240
ggaaggtttc cagggaagag gggactcagc aacgaggggt gctccctctg cagtntttat 300
tggaatagta ctggtacttt ttattgtagg tcgtcttntt tctagcaaaa cagggtngca 360
gcagccttat cacacttca c acagttgact tctgcaggag tccnttttt gcacaggttg 420
attctgctcc ccgaagttac taaacttttt tt 452
```

<210> 148

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. phospholipase a2,
group iia (platelets, synovial fluid) (PLA2G2A)
gene.

<400> 148

```
tggagtcctc tgagagagcc accaaggagg agcaggggag cgacggccgg ggcagaagtt 60
gagaccaccc agcagaggag ctaggccagt ccatctgc at ttgtcaccca agaactctta 120
ccatgaagac cctcctactg ttggcagtga tcatgatctt tggectactg caggcccatg 180
ggaatttgggt gaatttccac agaatgatca agttgacgac aggaaaggaa gccgcactca 240
gttatggctt ctacggctgc cactgtggcg tgggttgagc aggatcccc aaggatgcaa 300
cggattcgct gctgtg tcac tcatgactgt ttgtacaaa cgtctgggag aaacgtgggt 360
tnttggcacc aaatttttt 379
```

<210> 149

<211> 854

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(854)

<223> phospholipase a2, group iia (platelets,
synovial fluid) (PLA2G2A) gene.

<400> 149

```
gaattcccaa ctctggagtc ctctgagaga gccaccaagg aggagcaggg gagcgacggc 60
cggggcagaa gttgagacca ccagcagag gagctaggcc agtccatctg catttgtc ac 120
ccaagaactc ttacatgaa gaccctccta ctgttggcag tgatcatgat ctttggccta 180
ctgcaggccc atgggaattt ggtgaatttc cacagaatga tcaagttgac gacaggaaag 240
gaagccgcac tcagttatgg cttctacggc tgccactgtg gcgtgggtgg cagaggatcc 300
```

```
ccaaggatg caacggatcg ctgctgtgtc actcat gact gttgctacaa acgtctggag 360
aaacgtggat gtggcaccaa atttctgagc tacaagtta gcaactcggg gagcagaatc 420
acctgtgcaa aacaggactc ctgcagaagt caactgtgtg agtgtgataa ggctgctgcc 480
acctgttttg ctagaaacaa gacgacctac aataaaaagt accagtacta ttccaataaa 540
cactgcagag ggag caccctc tcgttctga gtccctctt ccctggaaac cttccacca 600
gtgctgaatt tccctctctc ataccctccc tccctaccct aaccaagttc cttggccatg 660
cagaaagcat ccctcaccca tcctagaggc caggcaggag cccttctata cccaccaga 720
atgagacatc cagcagattt ccagccttct actgctctcc tccacctcaa ctccgt gctt 780
aaccaaagaa gctgtactcc ggggggtctc ttctgaataa agcaattagc aaatcaaaaa 840
aaaaaaagga attc 854
```

<210> 150

<211> 224

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(224)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 150

```
ggttgagcac aggnacttt attgatgna catgacaagg tgcggctccc taggccctc 60
ccctnttcaa ggggtctaca tggcaact nt gaggagggga gattcagtgt ggtgggggac 120
tgagtntggc agggactccc cagcagttag ggtctctctc ttcctcttnt gctcttntctg 180
ggngtgggtg nccagggntn ttactccttg gaggccatnt gggc 224
```

<210> 151

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 151

```
gcgtgagta cgtcgtggag tccactggcg tcttcaccac catggagaag gctggggctc 60
atttgcaggg gggagccaaa agggatcatc tctctgcccc ctctgctgat gcccccatgt 120
tggtcatggg tgtgaaccat gagaagtatg acaacagcct caagatcatc agcaatgcct 180
cctgcaccac caactgctta gcaccctgg gccaaaggta tccatgacaa ctttggtatc 240
gtggaaggac tcatgaccac agtccatgcc atcactgcca c ccagaagac tgtggatggc 300
ccctncggga aactgtgggc gtgatggccg cgggggttctt tcagaacatc atccctgcc 359
```

<210> 152

<211> 1283

<212> DNA/RNA

102/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1283)

<223> glyceraldehyde -3-phosphate dehydrogenase
(GAPD) gene.

<400> 152

```
ctctctgctc ctctgttcg acagtcagcc gcatcttctt ttgcgtcgcc agccgagcca 60
catcgctcag acaccatggg gaagggtgaag gtcggagtca acggatttgg tcgtattggg 120
cgctgggtca ccagggtctg ttttaactct ggta aagtgg atattgttgc catcaatgac 180
cccttcattg acctcaacta catggtttac atgttccaat atgattccac ccatggcaaa 240
ttccatggca ccgtcaaggc tgagaacggg aagcttgtca tcaatggaaa tcccatcacc 300
atcttccagg agcgagatcc ctccaaaatc aagtggggcg atgctggcgc tgagtacgtc 360
gtggagtcca ctggcgtctt caccaccatg gagaaggctg gggctcattt gcagggggga 420
gccaaaaggg tcatcatctc tgcccoctct gctgatgcc ccattgttct catgggtgtg 480
aaccatgaga agtatgacaa cagcctcaag atcatcagca atgcctcctg caccaccaac 540
tgcttagcac ccctggccaa ggtcatccat gacaactttg gtatcgtgga agga ctcattg 600
accacagtcc atgccatcac tgccacccag aagactgttg atggccctc cgggaaactg 660
tggcgtgatg gccgcggggc tctccagaac atcatccctg cctctactgg cgctgccaag 720
gctgtgggca aggtcatccc tgagctgaac gggaagctca ctggcatggc cttccgtgtc 780
cccactgcca acgtgtcagt ggtggacctg ac ctgccgtc tagaaaaacc tgccaaatat 840
gatgacatca agaaggtggt gaagcaggcg tcggagggcc ccctcaaggg catcctgggc 900
tacactgagc accaggtggt ctccctctgac ttcaacagcg acacccactc ctccacctt 960
gacgtctggg ctggcattgc cctcaacgac cactttgtca agctcattc ctggtatgac 1020
aacgaatttg gctacagcaa cagggtgggt gacctcatgg ccacatggc ctccaaggag 1080
taagaccctt ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg 1140
ctggggagtc cctgccacac tcagtccccc accacactga atctccctc ctcacagttg 1200
ccatgtagac ccctgaaga ggggaggggc ctaggagacc gcacctgt c atgtaccatc 1260
aataaagtac cctgtgctca acc                                     1283
```

<210> 153

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 3' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 153

```
tacttaata gattcaatan aaagaacaaa cacacacaaa cacaacacg tcttaaaata 60
aactctttag agactaagtg cgtgtttctt ttccacagta cgggtgcagag aggggagggc 120
agggggcggg ggtcccttcc caatgtcccc gcggtgttga gta ccaggcg gcggggccag 180
ctccntant ncgccccctc ttccctctcc tgtaaatac acaaataat tatattcaat 240
ntgaatcng tctntttcca gcagaaaaaa aacatacaaa aaaaagtggg aagggggggg 300
cttntttaa cgttcgangg ttggaaggnc tttggggcnc aggggtaggg angggccgag 360
t                                     361
```

<210> 154

<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 5' terminal sequence. jun b proto -oncogene
(JUNB) gene.

<400> 154
agcgcatcaa agtngagcgc angccttgcg gaaccggctn gcggccacca agtgccggaa 60
gcggaantgg gagcgcatcg ggcttgggag gacaaggtga agacgctcaa ggccgagaac 120
gcgggntgt cgagtaccgc cggcttcctc cgggagcagg tggcccagct caaacagaag 180
gtcatgaccc acgtnagc aa cggctntnag ctgctgcttn ggtcaaggg acacgccttc 240
tggaacgttc cctgcccctt tacgggacac ccccttcgtt tnggacggtt nggcacacgg 300
tttcccaactn gggttccagg gtagcaggcg gtgggnnacc cacctggggg acntaggggg 360
cgncgcgaaa ccacattngg atttccggcc ttcttaacct t 401

<210> 155
<211> 1797
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1797)
<223> jun b proto-oncogene (JUNB) gene.

<400> 155
ccagcaggga gctgggagct gggggaaacg acgc caggaa agctatcgcg ccagagaggg 60
cgacgggggc tcgggaagcc tgacagggct tttgcgcaca gctgccggct ggctgctacc 120
cgcccgcgcc agcccccgag aacgcgcgac caggcaccca gtccggtcac cgcagcggag 180
agctcgccgc tcgtgcagc gagggccgga gcggcccgcc agggaccctc cccagaccgc 240
ctgggccgcc cgatgtgca ctaaaatgga acagcccttc taccacgacg actcatacac 300
agctacggga tacggccggg cccctggtgg cctctctcta cagactaca aactcctgaa 360
accgagcctg gcgtcaacc tggccgaccc ctaccggagt ctcaaagcgc ctggggctcg 420
cggacccggc ccagagggcg gcggtggcgg cagctacttt tctggtcagg gctcg gacac 480
cggcgcgtct ctcaagctcg cctcttcgga gctggaacgc ctgattgtcc ccaacagcaa 540
cggcgtgato acgacgacgc ctacaccccc gggacagtag ttttaccccc gcgggggtgg 600
cagcggtgga ggtgcagggg gcgcaggggg cggcgtcacc gaggagcagg agggcttcgc 660
cgacggcctt gtcaaagccc tggacgatct gca caagatg aaccacgtga cccccccaa 720
cgtgtccctg ggcgtaccg gggggccccc ggctggggcc gggggcgtct acgccggccc 780
ggagccacct cccgtttaca ccaacctcag cagctactcc ccagcctctg cgtcctcggg 840
aggcgcgggg gctgccgtcg ggaccgggag ctcgtaccgc acgaccacca tcagctacct 900
cccacacgcg ccgcccttcg ccggtggcca cccggcgcag ctgggcttgg gccgcggcgc 960
ctccaccttc aaggaggaac cgacagccgt gccggaggcg cgcagccggg acgccacgcc 1020
gccggtgtcc cccatcaaca tgaagacca agagcgcac aaagtggagc gcaagcggct 1080
gcggaaccgg ctggcgcca ccaagtgcg gaagcgggag ctggagcgca t cgcgcgcct 1140
ggaggacaag gtgaagacgc tcaaggccga gaacgcgggg ctgtcgagta ccgccggcct 1200
cctccgggag caggtggccc agctcaaaca gaaggtcatg acccagctca gcaacggctg 1260
tcagctgctg cttgggggtca agggacacgc cttctgaacg tcccctgccc ctttacggac 1320
accccctcgc ttggacggct gggcac acgc ctcccactgg ggtccagggg gcaggcgggtg 1380
ggacccacc ctgggaacct ggggcgcgc aaaccacact ggactccggc cccctaccc 1440

104/292

tgcgccagct ccttccacct cgacgtttac aagccccccc ttccactttt tttgtatgt 1500
tttttttctg ctggaaacag actcgattca tattgaatat aatatatttg tgtatttaac 1560
agggagggga agagggggcg atcgggcg agctggcccc gccgcctggt actcaagccc 1620
gcggggacat tgggaagggg acccccgcct cctgccctcc cctctctgca ccgtactgtg 1680
gaaaagaaac acgcacttag tctctaaaga gtttatttta agacgtgttt gtgtttgtgt 1740
gtgtttgttc tttttattga atctatttaa gtaaaaaaaa aattgggtct ttattaa 1797

<210> 156

<211> 335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(335)

<223> 3' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 156

aagcatttta ataaaattaa caaataaata ttctaaactg tataggctac agggacaaag 60
ggtagaagct agagggccag tctttcctgc tcaggccctc aagtcacctt tagagagacc 120
ctgctctggg ctggtttggg gctaggactg ctgacttggg gaggcgggga gtgaacccgg 180
aatgggtgat ctgggctctt gcagccattc ctctttgttg gtgtagggga ggagagaaga 240
ggtcaaagaa agcaagaccc tgcaagaggc atcccagtga ccccagaag tgactggggt 300
aaggggagcg ctatcctagg anggtggggg tgggt 335

<210> 157

<211> 481

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(481)

<223> 5' terminal sequence. cellular retinoic
acid-binding protein 2 (CRABP2) gene.

<400> 157

gcctggactt gtcttgggtt ccagaacctg acgaccggc gacgcgacgt ctct tttagc 60
taaaagacag tgtccagtgc tccagcctag gagtctacgg ggaccgcctc ccgcgccgcc 120
accatgccca acttctctgg caactggaaa atcatccgat cggaaaactt cgaggaattg 180
ctcaaagtgc tnggggtgaa tgtgatgctg aggaagattg ctgtggctnc agcgtccaag 240
ccagcagtng agatcaaaca ggaggagac act ttctaca tcaaaacctc caccaccgtg 300
cggcaccaca gagattaact tcaagggtng ggaggagttt gagggagcag antgtgggtg 360
gggaggccct gttaaggagc ngggtgaaat ggggagagtg aggattaaat ggtcttttga 420
gcagaagttc ctgaaggng aggggcccga agaentcttg gaccngagaa tttccccacg 480
t 481

<210> 158

<211> 969

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(969)

<223> cellular retinoic acid-binding protein 2
(CRABP2) gene.

<400> 158

```
agctttgggg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgctccagc ctaggagtct acggggaccg 120
cctcccgcgc cgccaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaaa 180
acttcgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgtgg 240
ctgcagcgtc caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaaggt tggggaggag tttgaggagc 360
agactgtgga tgggaggccc tgtaagagcc tggtgaaatg ggagag tgag aataaaatgg 420
tctgtgagca gaagctctg aagggagagg gcccgaagac ctggtggacc agagaactga 480
ccaacgatgg ggaactgac ctgaccatga cggcggatga cgttgtgtgc accaggggtct 540
acgtccgaga gtgagtggcc acaggtagaa ccgcggccga agcccaccac tggccatgct 600
caccgcctg cttcactgcc ccct ccgtcc caccctccctc ttctaggata gcgctcccct 660
taccacagtc acttctgggg gtacttgga tgctcttgcc aggtcttgcc tttctttgac 720
ctcttctctc ctccctaca ccaacaaaga ggaatggctg caagagccca gatcaccat 780
tcggggttca ctcccgcct cccaagtca gcagtcctag ccccaaacca gccagagca 840
gggtctctct aaaggggact tgagggcctg agcaggaaaag actggccctc tagcttctac 900
cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaaatgct 960
ttaaaaaaa
```

<210> 159

<211> 344

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 159

```
cgcgntgga ggggaggtgg ccccgntcc gccgangaan tgcgcccg cc acccgagag 60
cncnagagg gaccattgac cttgggctcc ccaggaag gccttctgat gctgctgatg 120
gccttggtga ccaggggaga ccctgtgaag ccgtctcggg gcccgctggg gacctgcacg 180
tgtgagagcc cacattgcaa ggggcctacc tgccgggggg cctgggtgca cagtagtgct 240
tgggtgcggg aggaggggag gcacccc cag ggaacattcg gggntgcggg aantttgcac 300
agggaagtct tgcagggggg gcgccccacc gatttcgttc aacc 344
```

<210> 160

<211> 416

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. activin a receptor
type ii-like 1 (ACVRL1) gene.

<400> 160
gtcagtctcc cggaaccagg actgttcatc cctcgaggag aagatcttga cggccacact 60
ctcaccgtgc cacaagcccc gccacacttc gccatagcgc cttttccccc acactccacc 120
aaggcaacct gccgtngcca ctgtcctctg caccagggaa ggggagccct gagccactcc 180
ctgtgggtgg cagtcaactgt ccagggaggt cccccaacat gctgttcgcc ctgcttcaga 240
tgcttttcag ggatgaggat gggattttcc cagcttcgct gttgcagggc cacgttgctt 300
tttccttgcc tncgttcggg acatggccac agggcccagg ggacaaccag g gggccacca 360
gggggnccag gcaanggcca agncacgggg ggcccagggt ttnaaggggc cagttt 416

<210> 161
<211> 1970
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1970)
<223> activin a receptor type ii-like 1 (ACVRL1)
gene.

<400> 161
aggaaacggt ttattaggag ggagtgggtg agctggggcca ggcaggaaga cgctggaata 60
agaaacattt ttgtccagc ccccatccca gtcccgggag gctgccgcgc cagctgcgcc 120
gagcgagccc ctcccgggt ccagcccgtt cgggggccgc gccggacc c agcccggcgt 180
ccagcgctgg cggtgcaact gcggccgcgc ggtggagggg aggtggcccc ggtccgccga 240
aggtagcgc cccgccacce gcagagcggg cccagaggga ccatgacctt gggctcccc 300
aggaaaggcc ttctgatgct gctgatggcc ttggtgacct agggagacct tgtgaagccg 360
tctcggggcc cgctgggtgac ctgcacg tgt gagagcccac attgcaaggg gcctacctgc 420
cggggggcct ggtgcacagt agtgcgtggt cgggaggagg ggaggcacc ccaggaacat 480
cggggctgcg ggaacttgca caggagctc tgcagggggc gccccaccga gttcgtcaac 540
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caacctcctt cggagcagcc gggaacagat ggccagctgg ccctgacctt gggccccgtg 660
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caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca 780
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cagaccccca ccatccctaa ccggtctggt gcagacccgg tcctctcagg cctagctcag 1680
atgatgcggg agtgctggtg cccaaacccc tctgcccagc tcaccgcgct gcggatcaag 1740
aagacactac aaaaaattag caacagtcca gagaagccta aagtgattca atagcccagg 1800

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agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatggtgcc 1860
ctatctgggt agaggtagtg tgagtgtggt gtgtgctggg gatgggcagc t gcgcctgcc 1920
tgctcgcccc ccagcccacc cagccaaaaa tacagctggg ctgaaacctg 1970

<210> 162

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. lim domain protein
(RIL) gene.

<400> 162

gtgacctgc gcgggccttc gccctggggc ttccgcctgg tngggccgng gacttcagcg 60
cgccctcac catctocagg gtccatgctg gcagcaaggc tcatntggct gccctgtgcc 120
caggagacct gatccaggcc atcaatggtg agagcacaga gctcatgac a cacctggang 180
cacagaaccg catcaagggc tgccacgac acctcacact gtctgtgagc aggcctgagg 240
gcaggagctg gcccagtgcc cctgatgaca gcaaggctca ggcacacagg atccacatcg 300
ntcctgagat ccaggacggc agcccaacaa ccagcaggcg gccctcaggc accgggactt 360
gggccagaag atnggcagan caagnct ggg gtttttncat atggaca 407

<210> 163

<211> 1130

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1130)

<223> lim domain protein (RIL) gene.

<400> 163

tgagagtccg gctcaggctc cggtgcggc tccagcccgc gatgcccacat tccgtgaccc 60
tgcgcgggcc ttccgcctgg ggcttccgcc tgggtgggccc ggacttcagc gcgcccctca 120
ccatctcacg ggtccatgct ggcagcaagg cctcattggc tgccctgtgc ccaggagacc 180
tgatccaggc catcaatggt gagagcacag agctcatgac acacctg gag gcacagaacc 240
gcatcaaggg ctgccacgat cacctocacac tgtctgtgag caggcctgag ggcaggagct 300
ggcccagtgcc ccctgatgac agcaaggctc aggcacacag gatccacatc gatcctgaga 360
tccaggacgg cagcccaaca accagcaggc ggccctcagg caccgggact gggccagaag 420
atggcagacc aagcctggga tctcc atatg gaaaaccccc ttgctttcca gtccctcaca 480
atggcagcag cgaggccacc ctgccagccc agatgagcac cctgcatgtg tctccacccc 540
ccagcgctga ccagcagag gectcccgcg gagccgggag cagagtcgac ctgggctccg 600
agggtgtacg gatgctgcgg gagccggccg agcccgtggc cgcggagccc aagcagtcag 660
gctccttccg ctacttgcat ggcatgtcag aggcgggcga gggcggggat tggcccgggc 720
ctggcgggccc ccggaacctc aagcccacgg ccagcaagct gggcgctccg ctgagcggcc 780
tgcaggggct gcccgagtgc acgcgtgct gccacggaat cgtgggcacc atcgtcaagg 840
aacgggacaa gctctaccat cccgagtgtc tcatgtgcag tgact gcggc ctgaacctca 900
agcagcgtgg ttacttcttt ctggacgagc ggctctactg tgagagccac gccaaaggcg 960
gcgtgaagcc gcccgagggc tacgacgtgg tggcggtgta ccccaatgcc aaggtggaac 1020
tcgtctgagc tgggacctg ctcccacccc tgcttcttaa ggtccctgct cggccggtgt 1080

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aaatatgttt caccctgtcc c tctaataaa gtcctctgc tcaaaaaaaaa

1130

<210> 164

<211> 310

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(310)

<223> 5' terminal sequence. shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 164

```
anattcgga  cgagggatcc  ctctatgtc  aacgtccaga  acctagacaa  ggcccggcaa  60
gcagtgggtg  gtgctgggcc  cccaatcct  gctatcaatg  gcagtgcacc  ccgggacctg  120
tttgacatga  agcccttcga  agatgctctt  cgcgctgc  ctc  cacctcccca  gtcggtgtcc  180
atgncctgagc  agctccgagg  ggagccctgg  gttccatggg  aagctgagcc  ggccgggaggc  240
tgaggcactg  ctggcagctt  caatggggat  ttccnggtac  gggagagcac  gaccacacng  300
gggcaatatg                                     310
```

<210> 165

<211> 3664

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3664)

<223> shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

<400> 165

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atggggcctg  aaactgtctg  ggtctgagct  ggggagcgga  agccacttgt  ccctctccct  60
ccccaggact  tctgtgactc  ctgggccaca  gaggtccaac  cagggttaag  gcctggggat  120
accccctgcc  tggccccctt  gccaaaactg  gcaggggggc  caggctgggc  agcagcccct  180
ctttcacctc  aactatggat  ctctgcccc  ccaagcccaa  gtacaatcca  ct  ccggaatg  240
agtctctgtc  atcgctggag  gaaggggctt  ctgggtccac  cccccggag  gagctgcctt  300
ccccatcagc  ttcatecctg  gggcccatcc  tgctcctct  gcctggggac  gatagtccca  360
ctacctgtg  ctcttcttc  ccccgatga  gcaacctgag  gctggccaac  ccgctgggg  420
ggcgccagg  gtctaagggg  gagccaggaa  gggcagctga  tgatggggag  gggatcgatg  480
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gaggcggcg  gcgcaggact  cgggtggaag  ggggccagct  tgggggcgag  gagtggacct  600
gccacgggag  ctttgtcaat  aagcccacgc  ggggctggct  gcatcccaac  gacaaagtca  660
tgggaccgg  ggtttcctac  ttggttcggt  acatgggttg  tgtggaggtc  ctccagtcaa  720
tgctgcccct  ggaattcaac  acccgactc  aggtcaccag  ggaggccatc  agtctggtgt  780
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tcagctctat  cctggggagg  agtaacctga  aatttgctgg  aatgccaatc  actctaccg  900
tctccaccag  cagcctcaac  ctcatggccg  cagactgcaa  acagatcatc  gcccaaccacc  960
acatgcaatc  tatctcattt  gcatccggcg  gggatccgga  cacagccgag  tatgtcgctt  1020
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ttgcccagga  tgcatcagc  accattg  gcc  aggccttcga  gttgcgcttc  aaacaatacc  1140
```

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```

tcaggaaccc acccaaaactg gtcaccacctc atgacaggat ggctggcttt gatggctcag 1200
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taggacagcc tgttggggga gatocagaag tccgaaaca gatgccacct ccaccacct 1440
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cccggcaagc agtgggtggt gctggggcccc ccaatcctgc tatcaatggc agtgaccccc 1560
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ggcctgtgag gtaactggga tcgcaccttt tataccagag acctgaggca gatgaaattt 3600
atttccatct aggactagaa aaacttgggt ctcttaccgc gagactgaga ggcagaagtc 3660
agcc 3664

```

<210> 166

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)
gene.

<400> 166

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```
gagcacaggg tcttttattg atggtacatg acaaggtgcg gctccctagg cccctcccct 60
cttcaagggg tctacatgga aactgtgagg aggggagatt cagtgtggtg ggggactgag 120
tntggcaggg actccccagc agtgagggtc tctctcttcc tcttgtgctc ttgctggggc 180
tggtggtcca ggggtcttac tccttgaggg ccatgtgggc atgaggtcca ccacctgtt 240
gctgtagcca aattcgttgt cataccaggg aaatgagctt gacaaagtgg tcgttgaggg 300
caatgccagc cccagccttc gaaggtggag gantgggttt cgctnttgaa gtcagaggag 360
accacctggg tgctcagttt agcccaggga tgcccttgag ggggccctcc gacgttt ttt 420
tcaccacctt tttgatntca tcatntttt 449
```

<210> 167

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(467)

<223> 5' terminal sequence.

glyceraldehyde -3-phosphate dehydrogenase (GAPD)
gene.

<400> 167

```
tggtcgacag tcagccgcat cttcttttgc gtcgccagcc gagccacatc gctgagacac 60
catggggaag gtgaaggctg gagtcaacgg atttggtcgt attgggcgcc tggtcaccag 120
ggctgctttt aactctggta aagtggata t tggtgccatc aatgaccctt tcattgacct 180
caactacatg gtttacatgt tccaatatga ttccacccat gggcaaattc catgggcacc 240
gtcaaggctg agaacgggaa gcttgtcatc aatgggaaat cccattcacc atcttcagg 300
gagcgagatc cctccaaaat tcaagtgggg ggcgatgctg ggcgcttgag ttacgttcgt 360
gggagtcca ctgggccttc tttcaaccac ccttgagagaa gggtttgggg gttcattttt 420
caaggggggg gagcccaaan ggtcttcat tttttggccc ccttttt 467
```

<210> 168

<211> 316

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(316)

<223> 3' terminal sequence. desmin (DES) gene.

<400> 168

```
ggcttgtgtt tnttntctct ttattgtttc tctccagagc ccctgcagca ggggagggga 60
gggcgtgggg aggtgggggc cctcccacc agcctgagac cgctctctgc ctctctctc 120
tcctctcttc tccagcatct cac ccacttt ctctcttctt naatctctctg ctcccacctc 180
cagcaccttc ggggattccc tctttagacc cctgctttct aagtcacccc ggggctgggg 240
aaaggaaaagt aagagaccac ggggacaatt tcaagcccc cagtntccac aggggctagt 300
ccctgggnt acctgc 316
```

<210> 169

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 5' terminal sequence. desmin (DES) gene.

<400> 169

```
atctcccat ccagacctac tctgccctca acttccgag a aaccagccct gagcaaaggg 60
gttctgaggt ccataccaag aagacggtga tgatcaagac catcgagaca cgggatgggg 120
aggtcgtcag tgaggccaca cagcagcagc atgaagtgt ctaaagacag agaccctctg 180
ccaccagaga ccgtcctcac ccctgtcctc actgctccct gaagccagcc ttcttccatc 240
ccagggacac cacacca gc cttcagtcct cccttcaca gctctggac ccctcctcac 300
tgggccattc cctcgtggtt ccccaacagc ggacataggc ccatccttgc tgggttcaca 360
ggggcatggc cccgggccac ttnttgctgg aacccagtt gttgaggtt tgggtgtttg 420
ggcagttgag ttgaggtttt 440
```

<210> 170

<211> 2218

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2218)

<223> desmin (DES) gene.

<400> 170

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gcctcgcgcg cgcgcgcacc atgagccagg cctactcgtc cagccagcgc gtgtcctcct 120
accgcgcgac ctccggcggc gccccgggct tcccgctcgg ctcccgcgtg agctcgcgcg 180
tggtccgcg ggccgggttt ggctotaagg gctcctccag ctccggtgacg tcccgcgtgt 240
accaggtgtc gcgcacgtcg ggccgggg ccg ggggcctggg gtcgctgcgg gccagccggc 300
tggggaccac ccgcacgccc tcctcctacg gcgcaggcga gctgctggac ttctcactgg 360
ccgacgcggt gaaccaggag ttctgacca cgcgcaccaa cgagaagtg gagctgcagg 420
agctcaatga ccgcttcgcc aactacatcg agaaggtgcg ctccctggag cagcagaacg 480
cgctcgcgcg cgaagtgaac cggtcaagg gccgcgagcc gacgcgagtg gccgagctct 540
acgaggagga gctgcgggag ctgcggcgcc aggtggaggt gctcactaac cagcgcgcgc 600
gcgtcgacgt cgagcgcgac aacctgctcg acgacctgca gcggtcaag gccagctgc 660
aggaggagat tcagttgaag gaagaagcag agaacaattt ggctgcc ttc cgagcggacg 720
tgatgcagc tactctagct cgcattgacc tggagcgcag aattgaatct ctcaacgagg 780
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ttgacgccct caagggcact aacgattccc tgatgaggca gatgcgggaa ttggaggacc 1140
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ggatcaatct ccccatccag acctactctg ccctcaactt ccgagaaacc agccctgagc 1380
aaaggggttc tgaggtccat accaagaaga cgggtgatgat caagaccatc gagacacggg 1440
atggggaggt cgtcagtgag gcgacacagc agcagcatga agtgctctaa agacgagaga 1500
ccctctgcc aagagaccg tcctcaccct tgcctcact gctcctgaa gccagcctt 1560
```

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```
cttccatccc agga caccac acccagcctc agtcctcccg tcacagcctc tgaccctcc 1620
tcactggcca tcctcgtgg tccccaacag cgacatagcc catccctgcc tggtcacagg 1680
catgccccgg ccacctctgc ggaccccagc tgtgagcctt ggctgttggc agtgagttag 1740
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gtgacctgag gcctacgctt tggctctgga gatagcccca gagcaggggtg ttgggatact 1860
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gtctcttact ttcctttccc cagcccag gg tggacttaga aagcaggggc tacaagaggg 2040
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tgctggagaa gagagaggag gagagaggca gagagcggtc tgaggctggt gggaggggag 2160
cccacctccc cagccctcc cccccctgc tgcaggggct ctggagagaa acaataaa 2218
```

<210> 171

<211> 367

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(367)

<223> 5' terminal sequence. casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 171

```
gatccacgac cgctacatcc ttaccaaccg tggcatcgcc agatgttggg aaagtaccag 60
caaggagact ttggttactg tcctcgtgtg tactgtgaga accagccaat gcttcccatt 120
ggcctttcag acatcccagg tgaagccatg gtgaagctct actgccccaa gtgcatggat 180
gtgtacacac ccaagtcacg aagacaccat cacacggatg ggcgcctac t ttcggcactg 240
gtttccctca catgctcttc atgggtgcat cccgagtacc ggcccaaggg gaccttgcca 300
accagtttgt gccaggggtt ttacggtttt caaggttcca tncgggtggg cttaccagggt 360
tgcagggt 367
```

<210> 172

<211> 1128

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1128)

<223> casein kinase 2, beta polypeptide (CSNK2B) gene.

<400> 172

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tgcgcgggtc atcctgggat tggtagttcg ctttctctca tttagccagt ttctttctct 120
accggggact ccgtgtcccg gcacccaccg cggcacctga cccttgccgc ttgcgtgttg 180
ccctcttccc caccctccct aatttcact cccccaccc cacttcgcct gccgcggtcg 240
ggtccgcggc ctgcgtgtga gcgg tcgccg ccgttccctg gaagtagcaa cttccctacc 300
ccacccagct cctgggtccc gtccagccgc tgacgtgaag atgagcagct cagaggaggt 360
gtcctggatt tcctggttct gtgggtccg tggcaatgaa ttcttctgtg aagtggatga 420
agactacatc caggacaaat ttaattctac tggactcaat gagcaggtcc ctcactatcg 480
acaagctcta gacatgatct tggacctgga gcctgatgaa gaactggaag acaaccccaa 540
```

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```
ccagagtgc ctgattgagc aggcagccga gatgctttat ggattgatcc acgcccgccta 600
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ttactgtcct cgtgtgtact gtgagaacca gccaatgctt ccca ttggcc tttcagacat 720
cccagtgaa gccatggtga agctctactg ccccaagtgc atggatgtgt acacacccaa 780
gtcatcaaga caccatcaca cggatggcgc ctacttcggc actggtttcc ctcacatgct 840
cttcatggtg catcccagat accggcccaa gagacctgcc aaccagtttg tgcccaggct 900
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caagagccca gtcaagacga ttcgtgatt cctccccc cctgtcctgc agtctttgtc 1020
tttcccttcc ttttttgcca ccttttcagg aacctgtat ggtttttagt ttaaattaaa 1080
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```

<210> 173

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 3' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 173

```
gggttttttt ctnaaaaaaa cctttgagtt gcaggtcagg tnagttgggt ctggaagtac 60
cggaagtctt gttggnatga gagagacttg tctacaggca ggnaaaccca agtttgccaa 120
acaaaggcag taaccccagc gaccagctgc tgctgtgca cgggtgaggag gaggaggaca 180
ccatggacac gagtggaggc tggatgggac aacgcagtgg acatctgcta atg ctctaac 240
acgggggttg ngtcacttct gagaagagcg aggttagtgg ggatnctata caagagggct 300
ntacaaactg gggcactggg atagggtagt tcctttgggn gggccaaggt gggctctacc 360
ccgtcctttg agctctngtg tncactnccg ttgggggatc cntcccaca cattcagggc 420
cantcaggna caattttacc aggtgntccc a ctgtttcac agggggattt aagtt 475
```

<210> 174

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. golgi apparatus
protein 1 (GLG1) gene.

<400> 174

```
ggatcatctt tgcctgaagc tgagatatgc tgaccagcgc ctgtottcag actgtgaaga 60
ccagatccga atcattatcc aggagtccgc cctggactac cgcctggatc ctcagctcca 120
gctgcactgc tcagacgaga tctccagtct atgtgctgaa gaagcagcag cccaagagca 180
gacaggtcag gtggaggagt gcc tcaaggt caacctgtc aagatcaaaa cagaattgtg 240
taaatnggaa gtgctaaaca tgctgaagga aagcaaaagca gacatctttg ttgacccggt 300
acttcatact tgcttgtgcc ctgggacatt aaacaccact gcgcagcatt caccctgggc 360
cgcgggcggt caaattgttc ctgtnttcat gggaaggcac tgggaggggt aaggcggtt 420
gaggtttaca gcccaggttg caaaaaggcg cttcattgac ccggtttgag gtgttggtt 480
ttt 483
```

<210> 175
<211> 3909
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc feature
<222> (1)..(3909)
<223> golgi apparatus protein 1 (GLG1) gene.

<400> 175
ggcacgaggc tcgccgcgga ctcaagatgg cggcgtgtgg acgtgtacgg aggatgttcc 60
gcttgtcggc ggcgtgcat ctgctgctgc tattcgcggc cgggggcaga aactccccgg 120
ccagggcgct ccac agccag ggccagggtc cgggggcaa ctttgtgtcc ttcgtagggc 180
aggccggaag cggcggcccg gcgggtcagc agctgcccc gctgcctcag tcatcgagc 240
ttcagcagca acagcagcag cagcaacagc aacagcagcc tcagccgccc cagccgcctt 300
tcccggcggg tgggcctccg cggcggggag gagcggggg tgggggggc tggaag ctgg 360
cggaggaaga gtcctgcagg gaggacgtga cccgcgtgtg ccctaagcac acctggagca 420
acaacctggc ggtgctcgag tgcctgcagg atgtgaggg gcctgaaaat gaaatttctt 480
cagactgcaa tcatttgttg tggaattata agctgaacct aactacagat cccaaatttg 540
aatctgtggc cagagaggtt tgcaaatcta ctat aacaga gattaaagaa tgtgctgatg 600
aaccggttgg aaaaggttac atggtttcct gcttagtgga tcaccgaggc aacatcactg 660
agtatcagtg tcaccagtac attaccaaga tgacggccat ctttttagt gattaccgtt 720
taatctgtgg cttcatggat gactgcaaaa atgacatcaa cattctgaaa tgtggcagta 780
ttcggcttgg agaaaaggat gcacattcac aaggtagggt ggtatcatgc ttggagaaaag 840
gcctggtgaa agaagcagaa gaaagagaac ccaagattca agtttctgaa ctctgcaaga 900
aagccattct cgggtggct gagctgtcat cggatgactt tcaacttagac cggcatttat 960
attttgcttg ccgagatgat cgggagcgtt tttgtgaaaa tacacaagct ggtg agggca 1020
gagtgtataa gtgcctcttt aaccataaat ttgaagaatc catgagttaa aagtgtcgag 1080
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ccaaatcctg taaaagtgc ttgaagaaat accggtgcaa tgtggaaaac cttccgcgat 1200
cgcgtgaagc caggctctcc tacttgta a tgtgcctgga gtcagctgta cacagagggc 1260
gacaagtcag cagtgagtg cagggggaga tgctggatta ccgacgcag ttgatggaag 1320
acttttctct gagccctgag atcatcctaa gctgtcggg ggagattgaa caccattgtt 1380
ccggattaca tcgaaaagga cggaccctac actgtctgat gaaggtagt cgaggggaga 1440
aggggaacct tggaatgaac tgccagcagg cgcttcaaac actgattcag gagactgacc 1500
ctggtgcaga ttaccgcatt gatcgagctt tgaatgaagc ttgtgaatct gtaatccaga 1560
cagcctgcaa acatataaga tctggagacc caatgatctc gtcgtgcctg atggaacatt 1620
tatacacaga gaagatggta gaagactgtg aacaccgtct ct tagagctg cagtatttca 1680
tctcccgga ttggaagctg gaccctgtcc tgtaccgcaa gtgccaggga gacgcttctc 1740
gtctttgcca caccacgggt tggaatgaga ccagtgaatt tatgcctcag ggagctgtgt 1800
tctcttgttt atacagacac gcctaccgca ctgaagaaca gggaaggagg ctctcacggg 1860
agtgcgagc tgaagtc caa aggatcctac accagcgtgc catggatgtc aagctggatc 1920
ctgccctcca ggataagtg ctgattgac tgggaaaatg gtgcagtga aaaacagaga 1980
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tgagagcctg tgagcccata attcagacat tctgccacga tgcggataac cagatagact 2160
ctggggacct gatggagtgt ctgatacaga acaaacacca gaaggacatg aacgagaagt 2220
gtgccatcgg agttaccac ttccagctgg tgcagatgaa ggattttcgg ttttcttaca 2280
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tggacgtggt gatctgcctg agcacgaccg tgcgcaatga cactctgcag gaagccaagg 2400
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gttccgctgt gcaatatggc aacgctcaga ttatcgaatg tctgaaagaa aacaagaagc 2580
agctaagcac ccgctgccac caaaaagtat ttaagctgca ggagacagag atgatggacc 2640
cagagctaga ctacacctc atgagggtct gcaagcagat gataaagagg ttctgtccgg 2700

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```

aagcagattc taaaaccatg ttgcagtgc tgaagcaaaa taaa aacagt gaattgatgg 2760
atcccaaatg caaacagatg ataaccaagc gccagatcac ccagaacaca gattaccgct 2820
taaaccccat gttaagaaaa gcctgtaaag ctgacattcc taaattctgt cacggtatcc 2880
tgactaaggc caaggatgat tcagaattag aaggacaagt catctcttgc ctgaagctga 2940
gatatgctga ccagcgccct g tcttcagact gtgaagacca gatccgaatc attatccagg 3000
agtcgcgcct ggactaccgc ctggatcctc agctccagct gcaactgctca gacgagatct 3060
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caaccccggt ttagagcatt agcagatgtc cactgcgttg tcccatccag cctccactcg 3720
tgtccatggt gtctctctcc tctcaccgt gcagcagcag cagctggtcg ctgggggttac 3780
tgctcttggt tggcaaacct gggtttacct gcctgtagac aagtct ctct cataccaaca 3840
gaacttcggt tacttcaga accaactcac ctgacctgca actcaaaggc ttttttaaga 3900
aaaccacca                                     3909

```

<210> 176

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(390)

<223> 5' terminal sequence. endothelin receptor
type b (EDNRB) gene.

<400> 176

```

gttaagatca aacctcaca agagaaatag aatgtttgaa aggctatccc aaaagacttt 60
tttgaatctg tcattcacat accctgtgaa gac aatacta tctacaattt tttcaggatt 120
attaaaatct tcttctttca ctatcgtagc ttaaactctg tttggttttg tcatctgtaa 180
atacttaoct acatacactg catgtagatg attaaatgag ggcaggccct gtgctcatag 240
ctttacgatg gagagatgcc agtgacctca taataaagac tgtggaactg cctgggtgca 300
gtgtccacat gacaaagggg caggtaggca ccctctcttc acctatgctg tgggttaaat 360
gggtttctag gcatatgtat tatggctatt                                     390

```

<210> 177

<211> 4286

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4286)

<223> endothelin receptor type b (EDNRB) gene.

<400> 177

gagacattcc ggtgggggac tctggccagc ccgagcaacg tggatcctga gagcactccc 60
 aggtaggcat ttgccccggt gggacgcctt gccagagcag tgtgtggcag gcccccggtg 120
 aggatcaaca cagtggctga ac actgggaa ggaactggta cttggagtct ggacatctga 180
 aacttggctc tgaaactgcg cagcgccac cggacgcctt ctggagcagg tagcagcatg 240
 cagccgcctc caagtctgtg cggacgcgc ctggttgccg tggttcttgc ctgcgccctg 300
 tcgcgatct ggggagagga gagaggcttc ccgcctgaca gggccactcc gcttttgcaa 360
 accgcagaga taatgacgcc acccactaag accttatggc ccaagggttc caacgccagt 420
 ctggcgcggt cggtggcacc tgcggagggt cctaaaggag acaggacggc aggatctccg 480
 ccacgcacca tctccccctc cccgtgcca ggaccatcg agatcaagga gacttttcaa 540
 tacatcaaca cggttgtgtc ctgccttgtg ttctgtgtgg gg atcatcgg gaactccaca 600
 ctcttgagaa ttatctacaa gaacaagtgc atgcgaaacg gtcccaatat cttgatcgcc 660
 agcttggctc tgggagacct gctgcacatc gtcattgaca tccctatcaa tgtctacaag 720
 ctgctggcag aggactggcc atttggagct gagatgtgta agctggtgcc tttcatacag 780
 aaagcctccg tgggaatcac tgtgctgagt ctatgtgtc tgagtattga cagatatcga 840
 gctgttgcct cttggagtag aattaaagga attggggttc caaatggac agcagtagaa 900
 attgttttga tttggctggt ctctgtgtcc ctgaagccat aggttttcat 960
 ataattacga tggactacaa aggaagttat ctgcgaatct gottgcttca tccggttcag 10 20
 aagacagctt tcatgcagtt ttacaagaca gcaaaagatt ggtggctgtt cagtttctat 1080
 ttctgcttgc cattggccat cactgcattt tttatacac taatgacctg tgaaatgttg 1140
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 gccaaaaccg tcttttgctt ggtccttgtc tttgccc tct gctggcttcc ccttcacctc 1260
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 aagttcaaaag ctaatgatca cggatatgac aacttccgtt ccagtaataa atacagctca 1560
 tcttgaagaa agaactatct actgtatttc attttcttta tattggaccg aagtcattaa 1620
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 taaaatatta agtgaatta ttttaacact cacagctaca tatgacattt tatgagctgt 1740
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 tttttacagt tagcacttca acatagctct taacaacttc caggatattc acacaacact 1860
 taggcttaaa aatgagctca ctacg aattt ctattcttcc taaaaagaga tttattttta 1920
 aatcaatggg actctgatat aaaggaagaa taagtccactg taaaacagaa cttttaaatg 1980
 aagcttaaat tactcaattt aaaattttta aatcctttta aacaactttt caattaatat 2040
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 ctgcatgtag atg attaaat gagggcaggc cctgtgctca tagctttacg atggagagat 2580
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 gcaggtagca ccctctctca cccatgctgt ggttaaaatg gtttctagca tatgtataat 2700
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 taaagcttat tactaatttt tgtattattt ttgtaaatag ccaatagaaa agtttgcttg 2820
 acatggtgct tttctttcat ctagaggcaa aactgctttt tgagaccgta agaacctctt 2880
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 gggttggagg aaacccatgg ggacagattc ccattcttag cctaacgttc gtcattgcct 3060
 cgtcacatca atgcaaaaagg tctgatattt gttccagcaa aacacagtg aatgttctca 3120
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 ttgttttctg tcaattatga atgtgatggt acagtaaacc aaaacccaac aatgtggcca 3300
 gaaagaaaga gcaataataa ttaattcaca caccatattg attctattta taaatcacc 3360
 acaacttgt tctttaattt catcccaatc actttttcag aggcctgtta tcatagaagt 3420
 cattttagac tctcaatttt aaattaattt tgaatcacta atattttcac agtttattaa 3480
 tatatttaat ttctatttaa atttttagatt atttttatta ccatgtactg aatttttaca 3540
 tctgatacc ctttcttctt ccatgtcagt atcatgttct ctaattatct tgccaaaattt 3600
 tgaaactaca caca aaagc atacttgcatt tatttataat aaaattgcat tcagtggctt 3660

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tttaaaaaaa atgtttgatt caaaacttta acatactgat aagtaagaaa caattataat 3720
ttctttacat actcaaaacc aagatagaaa aagggtgctat cgttcaactt caaaacatgt 3780
ttcctagtat taaggacttt aatatagcaa cagacaaaat tattgttaac atgg atgta 3840
cagctcaaaa gatttataaa agattttaac ctattttctc ccttattatc cactgctaata 3900
gtggatgtat gttcaaacac cttttagtat tgatagctta catatggcca aaggaatata 3960
gtttatagca aaacatgggt atgctgtagc taactttata aaagtgtaat ataacaatgt 4020
aaaaaattat atatctggga ggatttttt g gttgcctaaa gtggctatag ttactgattt 4080
tttattatgt aagcaaaacc aataaaaatt taagtttttt taacaactac cttattttttc 4140
actgtacaga cactaattca ttaaatacta attgattgtt taaaagaaat ataatgtga 4200
caagtggaca ttatttatgt taaatataca attatcaagc aagtatgaag ttattcaatt 4260
aaaatgccac atttctggtc tctggg 4286

```

<210> 178

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 3' terminal sequence. gran zyme b (granzyme
2, cytotoxic t-lymphocyte-associated serine
esterase 1) (GZMB) gene.

<400> 178

```

acancagaga tccatttatt acagtctgtc aaccocgact gccacccct tgggaattct 60
tgccctctgtc ccagagatgg tcaggcccag aggaagggtta gtctcatgcc tgctgttaga 120
ggcgnttcat tgttctcttt atccagggca ggaagtntga gacctgatg tagactcctg 180
gggggtgtccc tttttgttt ccataggaga gaataccttg ggctangtcc ttacananga 240
ggggccccc ggagttcccc cttgaaaccg gtctgtgtct tctttggatc cccacacaa 300
atntcagtgg gctctgctgt aattgccatg ggaaggagac gggtcac ant gggcagttcc 360
ttctgcactn ttcagggaaca atttctgaa gtgtgggttg ctaaagtgtc cattgagaaa 420
taaccocagg ccaggccaaa ttgaaaagtt gcctgggntt tt 462

```

<210> 179

<211> 960

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(960)

<223> granzyme b (granzyme 2, cytotoxic
t-lymphocyte-associated serine esterase 1) (GZMB)
gene.

<400> 179

```

agcagctcca accagggcag ctttctgag aagatgcaac caatcctgct tctgctggcc 60
ttcctcctgc tgcccagggc agatgcaggg gagatcatcg ggggacatga ggccaagccc 120
cactcccgcc cctacatggc ttatcttatg atctgggatc agaagtctct gaagaggtgc 180
ggtggcttcc tgatacaaga cgacttcgtg ctgacagctg ctactgttg gggaagctcc 240
ataaatgtca cttggggggc ccacaatatc aaagaacagg agcc gaccca gcagtttatc 300
cctgtgaaaa gaccatccc ccatccagcc tataatccta agaacttctc caacgacatc 360

```


118/292

atgctactgc agctggagag aaaggccaag cggaccagag ctgtgcagcc cctcaggcta 420
cctagcaaca aggccaggt gaagccaggg cagacatgca gtgtggccgg ctgggggcag 480
acggccccc tgggaaaaca ct cacacaca ctacaagagg tgaagatgac agtgcaggaa 540
gatcgaaagt gcgaatctga cttacgccat tattacgaca gtaccattga gttgtgcgtg 600
ggggaccag agattaaaaa gacttccttt aagggggact ctggaggccc tcttgtgtgt 660
aacaagggtg cccaggggcat tgtctcctat ggacgaaaca atggcatgcc tccacgagcc 720
tgcaccaaag tctcaagctt tgtacactgg ataaagaaaa ccatgaaacg ctactaacta 780
caggaagcaa actaagcccc cgctgtaatg aaacaccttc tctggagcca agtccagatt 840
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agtccagatt tacactggga gaggtgccag caactgaata aa tacctctt agctgagtgg 960

<210> 180

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 3' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 180

tnaagcagca gcaattttta ttgagggacc taaactgaaa ataggttttag aacataatTT 60
aaaaaaataa aacagcaaaa gtagcaaaaa atatatgacc tttttaaaaa cattttcctt 120
ttttttcttt ttgtttttta atatatagca actga tgcct cccagccacc agngcatct 180
taccgatgg gtaaatctct ggtaacgacc cttttaaaaa gacatgtaaa tatatactca 240
gntttataca ctttgtgttt tcttcatagc tatntacaga gccccagtt tgggctgggc 300
caggggccaan caaactgcc cccaacctgg gccttcgcct caccatcctc tgggtaccgg 360
gcntttgggt caggcaaaag aaactagTnt cgggtttatt angccactgg naccacTTt 420
ttgggggcag aggtcacctt cattcgaggg cacgangcac tgacctcctt t 471

<210> 181

<211> 463

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(463)

<223> 5' terminal sequence. fibroblast growth
factor receptor 1 (fms-related tyrosine kinase 2,
pfeiffer syndrome) (FGFR1) gene.

<400> 181

gctttgctgc cagccacttc atccccctccc agatgttTga ccaacacccc tccttgcac 60
caggactgcc tganTggagg agtgggagcc aatgaacagg catgcaagtg agagcttct 120
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ttgctttgct gaccaaatgc ctgggtacca gaggatggTg aggcgaaggc aggttggggg 360
cagtgtTgtg gccngggggc agcccaaaac tgggggcttc tgtatatagc tattgaagaa 420

aacacaaatg tattaatctg agtatatatt ttacatgtnt ttt

463

<210> 182

<211> 4066

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4066)

<223> fibroblast growth factor receptor 1

(fms-related tyrosine kinase 2, pfeiffer syndrome)

(FGFR1) gene.

<400> 182

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<210> 183

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(415)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), catalytic subunit, alpha isoform
(PPP2CA) gene.

<400> 183

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tgattaaatg tctcagaaat atcttgccca aagggtgtaac cagctcctcg aggagatata 120
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ggaacttctt gtaggcgac aagtgtctctg atatgatcca gtgtat ctat agatggcgag 240
agaccaccat gtagacagaa gatctgcccc tccaccaagg cagtgaagg aagatagtca 300
aaaagatctg taaaatattt ccaaacattt gccatttcca tattttctta aacattcatt 360
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<210> 184

<211> 2181

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

121/292

<220>

<221> misc_feature

<222> (1)..(2181)

<223> protein phosphatase 2 (formerly 2a),
catalytic subunit, alpha isoform (PPP2CA) gene.

<400> 184

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agacttaatt gtaaaacat ataacttgag atttaagtct ttgggttggt ttttaataaa 2160
acagcatgtt ttcaggtaga g 2181
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<210> 185

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(375)

<223> 5' terminal sequence. homo sapiens, clone
image:4054156, mrna, partial cds (EST R55460)
gene.

122/292

<400> 185
cgaagaggat gaggaagagc tinctgtgct gcancaagag ctccaggccg ggctgcgcac 60
caaggccctg attgtggatg agtcctgccg gcggnacca tcttccaaca tagggatata 120
cctccctcct tcttataact gaagatcctg gagcccgaa gattcag ggc agacagaccc 180
tgataatgag cctggcaggg aagggaacc aacatcttgt aacttgcttt cccaccctg 240
tttctggggg cagagcaatt gcccaatttc taccctaate caaagtcctt ggggtgnggt 300
gggggttaaac gtgctgggtgc atcctagggtc atccaagagt gaggcgcaa gttcctgagg 360
aagggggcac agaac 375

<210> 186

<211> 542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(542)

<223> 3' terminal sequence. immunoglobulin kappa
constant (IGKC) gene.

<400> 186
gcaaagattc acaatattta ttnattctcc tccaacatta gcataattaa agccaaggag 60
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gggcacttct ccttctaaca ctctcccctg ttgaagctct ttgtgacggg cgagctcagg 240
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tggggataga agttttttca gcaggcacac aacagaggca nttccagatt tncaactgct 480
catcatgag cggggaagnt gaaggnacgt nggtgcagcc acatttctt tgatccncca 540
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<210> 187

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(296)

<223> 5' terminal sequence. melanocortin 1
receptor (alpha melanocyte stimulating hormone
receptor) (MCLR) gene.

<400> 187
atcacctgca gctccatgct gtccagcctc tgcttctgtg gcgccatcgc gtggaccgct 60
acatctccat cttctacgca ctgnctacca cagcatcgtg accctgccgc gggcgcaag 120
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gaccagtgg ccgtcctgct gtgcctcgtg gtcttcttcc tggctatgct ggtgctcatg 240
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<210> 188

123/292

<211> 1270
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1270)
<223> melanocortin 1 receptor (alpha melanocyte
stimulating hormone receptor) (MC1R) gene.

<400> 188
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accaagggcc ccctggcagc accatgaact aagcaggaca cctggagggg aagaactgtg 120
gggacctgga ggcctccaac gactccttcc tgcttctgga acaggactat ggctgtgcag 180
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agtgttgaag 1270

<210> 189
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(336)
<223> 3' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 189
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gcctcgtct ccggcgagat gtccgagcgc aaagaaggca gaggcaaagg gaagggcaag 120
aagaaggagc gaggctcgnc aagaagccgg ntccgcgggc ggngcagcag gagcccagcc 180
ttgcctcccc aattnaaaga gatgaaaagc caggaatcgg ctgcaggttc caaactagtc 240
cttcggtgtg aaaccagttc tgaatactcc tctctcagat tcaagtgggt caagaatggg 300
gaatgaattg aatcgaaaaa nncannccac aaaatt 336

124/292

<210> 190
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(366)
<223> 5' terminal sequence. neuregulin 1 (NRG1)
gene.

<400> 190
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cattctcggg gggtnngtta g gatggtgag gccattggc aatgttcac atattgtttc 120
gttcagaccg aagctctgcc agagacggtc atgcagcttt ttccgctgtt tcttggtttt 180
gcagtaggcc accacacaca tgatgccgac cacaaggagg gcgatgcaga tgccggttat 240
ggtcagcaact ctcttctggt acagctcctn cgcctncata aattcaatnc caagatgctt 300
gtagaagctg gccattnacg tagttttttg gcagcgattc accagtaaaa cttcatttng 360
gggcac 366

<210> 191
<211> 2490
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2490)
<223> neuregulin 1 (NRG1) gene.

<400> 191
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caggacggtg ataacctctc cccgatcggg ttgcgagggc gccgggcaga ggccaggacg 180
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gcggaaaaag ctgcatgacc gtcttcggca gagccttcgg tctgaacgaa acaatatgat 1320
gaacattgcc aatgggcctc accatcctaa cccaccccc gagaatgtcc agctggtgaa 1380

125/292

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tcctagccac agctggagca acggacacac tgaaagcatc ctttccgaaa gccactctgt 1560
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gtttgaccaa caccctcagc agttcagctc ctccaccac aaccocgcgc atgacagtaa 1980
cagcctccct gctagcccct tgaggatagt ggaggatgag gagtatgaaa cgaccaaga 2040
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caagccaat ggccacattg ctaacagatt ggaagtggac agcaacacaa gctcccagag 2160
cagtaactca gagagtgaaa cagaagatga aagagtaggt gaagatacgc ctttcctggg 2220
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caggactaac ccagcaggcc gcttctcgac acaggaagaa atccaggcca ggctgtctag 2340
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tgtaaaactt tattttatat aataaagtat tccaccttaa attaaacaat ttattttatt 2460
ttagcagttc tgcaataaaa aaaaaaaaaa 2490

```

<210> 192

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. ciliary neurotrophic
factor receptor (CNTFR) gene.

<400> 192

```

cagatgctac gccgggaagg agtacattat ccagggtggca gccaaaggaca atnagattgg 60
gacatggagt gactggagcg taccgccac gctacgccct ggactgagga accgcgacac 120
ctcaccacgg aggccaggc tgcggagacc acgaccagca ccaccagctc cctggcaccc 180
ccacctacca cgaagatctg tgaccctggg gagctgggca gcggcggggg accctcggca 240
cccttcttgg tcagcgtecc catcactctg gccctggctg ncgctgccgc cactgccagc 300
agtctcttga tctgagcccg gcaccccatg aggacatgca gagcacctgc agaggancag 360
gaggccggag cttgagcctt gtagacccg gtttctattt t ncacacggg caggaggant 420
tttgcattn tttttnagac acaatttttt gga 453

```

<210> 193

<211> 1566

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1566)

<223> ciliary neurotrophic factor receptor (CNTFR)
gene.

<400> 193

126/292

```

gcggcgccag cggaggcgcc ggctccagcc ggcgcgccgc gaggctcggc ggtgggatcc 60
ggcgggcggt gctagctccg cgctccctgc ctgcctcgtc gccggggcg gtcggaaggc 120
gcggcgccgaa gcccggttg cccgaggcg cgactct agc cttgtcacct catcttgccc 180
ccttggtttt ggaagtccct aagagttggt ctggaggagg aggaggacat tgatgtgctt 240
ggtgtgtggc cagtgttgaa gagatggctg ctccctgtcc gtgggcctgc tgtgtgtg 300
ttgcgcgcgc cgccgcagtt gtctacgcc agagacacag tccacaggag gcaccccatg 360
tgcagtacga gcgcc tgggc tctgacgtga cactgccatg tgggacagca aactgggatg 420
ctgcggtgac gtggcggtta aatgggacag acctggcccc tgacctgctc aacggctctc 480
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tctgtgagaa ggacccagcc ctcaagaacc gctgccacat tcgctacatg cacctgttct 780
ccaccatcaa gtacaaggtc tccataagtg tcagc aatgc cctggggccac aatgccacag 840
ctatcacctt tgacgagttc accattgtga agcctgatcc tccagaaaat gtggtagccc 900
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agacacaatt tgtggagacc ccggcgggcc cgggcctgcc gccccccagc cctgccgcac 1560
caagct 1566

```

<210> 194

<211> 349

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(349)

<223> 5' terminal sequence. angiogenin,
ribonuclease, rnase a family, 5 (ANG) gene.

<400> 194

```

ccgtgtacac aactcacac aaggacgcca accccaccta gatgcaaaga ggattcaaaa 60
gaacatcttt gcgttttcta ccggctcccc atcatcgtac tagggaggaa gaagcgggtg 120
agaaacaaaa cttctttcca ttgtcctgcc cgtttctgcg gacttgttct gaggccgagg 180
agcctgtggt ggaagagatg gtgatgggcc tgggcgtttt gttgttggtc ttctgtgctg 240
gtctgggtct gacccaccg accctggctc aggataactn c aggtacaca cacttctga 300
cccagcacta tgatgcaaaa ccacagggcc ngggatgaca gatactgtg 349

```

<210> 195

<211> 729

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

127/292

<221> misc_feature

<222> (1)..(729)

<223> angiogenin, ribonuclease, rnase a family, 5
(ANG) gene.

<400> 195

```
atgatgccgt gtcagagagc aaagctcctg tccttttggc ctaatttggg gatgctgttc 60
ttgggtctac cacacctcct tttgccctcc gcaggagcct gtgttggaag agatggtgat 120
gggcctgggc gttttgttgt tggctctcgt gctg ggtctg ggtctgacct caccgacct 180
ggctcaggat aactccaggt acacacactt cctgacctag cactatgatg ccaaaccaca 240
gggcccggat gacagatact gtgaaagcat catgaggaga cggggcctga cctcaccctg 300
caaagacatc aacacattta ttcatggcaa caagcgcagc atcaaggcca tctgtgaaaa 360
caagaatgga aa ccctcaca gagaaaacct aagaataagc aagtcttctt tccaggtcac 420
cacttgcaag ctacatggag gttccccctg gcctccatgc cagtaccgag ccacagcggg 480
gttcagaaac gttgtgtgtg cttgtgaaaa tggcttacct gtccacttgg atcagtcaat 540
tttccgtcgt ccgtaaccag cgggccccctg gtcaagtgtt ggctctgctg toct tgcctt 600
ccatttcccc tctgcacca gaacagtggg ggcaacattc attgccaagg gcccaaagaa 660
agagctacct ggaccttttg tttctgtttt gacaacatgt ttaataaata aaaatgtctt 720
gatatcagt                                     729
```

<210> 196

<211> 452

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(452)

<223> 3' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 196

```
ngttactcca gccttggacc ggggctgcc a tt ggagagn cgtggcgacc acaaggaggc 60
gcacatcctg aggttcctgc cgggcoactc ggcgggcccc ggacgggtga cgggtgaagg 120
ggaactgagc tgcgcacccg gggatctcga tgccgtcctc atcctgcagg gtccccctta 180
cgtgtcctgg ctcatcgacg ccaaccacaa catgcagatc tggaccactg gagaatactc 240
cttcaagatc tttccagaga aaaacattcg tggcttcaag ctcccagaca cacctcaagg 300
cctcctgggg ggacgcgngn atgcttcaat gccagcattg tggcatcctt cgtgggagct 360
taccgtggg ccagcattgt cttnatattca ttgccttcca gcttgcggtt gttagggttg 420
cagaccttaa cccgnaccgt ttccagacca tt                                     452
```

<210> 197

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. endoglin
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 197

128/292

```
aggacgagc ctttgcttgt gcaaccagac aggtcagggc tgatgatgtt caagcgcatg 60
aagacagtcc tatggcttcc tggctcttgag acccggtctt gggacgcagg gctaccgtgc 120
agctgagggg gccggttttg ggtatgggta ctgtgtagaa gtggaggagg aagctgaagc 180
gcgggtcacc ctcggggctt ggggacagca ggct cacaca gttgcccttg gccgcccgcc 240
cctgggatga gttccacggg gcctccctca ggccccaagt ccagggtggc agctgtctaa 300
ctggagcagg aactcggaga cggatgggga cantctgacc tgcacaaagc ttttnttgcc 360
ccggcttcga tgggtgtttt                                     379
```

<210> 198

<211> 3142

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3142)

<223> endoglin (osler-rendu-weber syndrome 1)
(ENG) gene.

<400> 198

```
cctgggcccg ccgggctgga tgagccgg ga gctccctgct gccggtcata ccacagcctt 60
catctgcgcc ctggggccag gactgtgct gtcactgcc tccattggag ccagcaccc 120
cctccccgcc catccttcgg acagcaactc cagcccagcc ccggtccct gtgtccactt 180
ctctgacc ctggccgccc acccagaag gctggagcag ggacgcgctc gctccggccg 240
cctgctcccc tgggtccccc gtgcgagccc acgccggccc cggtgcccgc ccgcagccct 300
gccactggac acaggataag gccagcgca caggcccca cgtggacagc atggaccgcg 360
gcacgctccc tctggctgtt gccctgctgc tggccagctg cagcctcagc cccacaagtc 420
ttgcagaaac agtccattgt gaccttcagc ctgtgggccc cgagagggg c gaggtgacat 480
ataccactag ccaggctctg aagggtcgcg tggctcaggc ccccaatgcc atccttgaag 540
tccatgtect ctctctggag ttcccaacgg gcccgtcaca gctggagctg actctccagg 600
catccaagca aaatggcacc tggcccgag aggtgcttct ggtcctcagt gtaaacagca 660
gtgtcttctt gcatctccag gccctgg gaa tccactgca cttggcctac aattccagcc 720
tggtcacett ccaagagccc ccgggggtca acaccacaga gctgccatcc ttccccaaga 780
cccagatcct tgagtgggca gctgagagg gcccacac cttgtgtgct gagctgaatg 840
accccagag catcctctc cgactgggcc aagcccagg gtcactgtcc ttctgcatgc 900
tggaagccag ccaggacatg ggccgcagc tcgagtggcg gccggtact ccagccttgg 960
tccggggctg ccacttgga ggctggccg gccacaagga ggcgacatc ctgagggtcc 1020
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ccggggatct cgatgcgctc ctcatctgc aggtccccc ctacg tgtcc tggctcatcg 1140
acgccaacca caacatgcag atctggacca ctggagaata ctcttcaag atctttccag 1200
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gcaaaggcct cgtcctgccc gccgtgtgg gcatcacctt tgggtgccttc ctcatcgggg 2160
ccctgctcac tgctgcactc tggtagatct actgcacac gcgtgag tac cccaggcccc 2220
```

129/292

```

cacagtgagc atgccgggcc cctccatcca cccgggggag ccagtgaa cctctgagg 2280
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ccccagcaa gcgggagccc gtggtggcgg tggctgcccc ggctcctcg gagagcagca 2400
gcaccaacca cagcatcgga a gcacccaga gcacccctg ctccaccagc agcatggcat 2460
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tgaacctga aaaaaaaaaa aa 3142

```

<210> 199

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(402)

<223> 3' terminal sequence. epidermal growth
factor (beta-urogastrone) (EGF) gene.

<400> 199

```

tatgtttttg gtgattttat ttaaataatt agaagaaatt catcgttgtc tataatgaaa 60
acaaatcagg caatttactt acaatcttgt aactgaaaat acatacaaa t tctgtgcaat 120
cacaccaaga gggaaaattc tgtaggggaa aaggacagta atgactaaga aactccgaag 180
cctcctgtgt aatattttta aaataaaatg ttttcattca aatattttta aaaataagcc 240
atctaattct gaagaaatca gtttctaat tacatttttc attgattcat cacaactcat 300
tttgcaaaat catcagcatg gaccacg cca atgaggagtt aaatgcctac actgtatctt 360
aacggtattg taatattcca atcatttcat gaaactgata ta 402

```

<210> 200

<211> 4877

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4877)

<223> epidermal growth factor (beta-urogastrone)
(EGF) gene.

<400> 200

```

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agctggaact ttccatcagt tcttcttttc ttttctctct ctaagccttt gccttgcctc 120
gtcacagtga agtcagcca g agcagggtg ttaaactctg tgaaatttgt cataagggtg 180
tcaggatatt ctactggct tccaaagaaa catagataaa gaaatctttc ctgtggcttc 240

```

ccttggcagg ctgcattcag aaggtotctc agttgaagaa agagcttggg ggacaacagc 300
 acaacaggag agtaaaagat gcccaggggc tgaggcctcc gctcaggcag ccgcatctgg 360
 ggtcaatcat actcaccttg cccggggccat gctccagcaa aatcaagctg ttttcttttg 420
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 catcgtggtg gctgtctgcg ttgtggtgct tgtcatgctg ctctcctga gctgtgggg 3600
 ggcccaactac tacaggactc agaagctgct atcgaaaaac ccaaagaatc cttatgagga 3660
 gtcgagcaga gatgtgagga gtcgcaggcc tgctgacact gaggatggga tgtcctcttg 3720
 ccctcaacct tggtttgtgg ttataaaaga acaccaagac ctcaagaatg ggggtcaacc 3780
 agtggctggg gaggatggc aggcagcaga tgggtcaatg caaccaactt catggaggga 3840
 ggagcccccag ttatgtggaa tgggcacaga gcaaggctgc tggattccag tatccagtga 3900

131/292

```

taagggtcc tgtccccagg taatggagcg aagctttcat atgcoctcct atgggacaca 3960
gaccttgaa ggggtgtcg agaagcccca ttctctcta tcagtaacc cattatggca 4020
acaaagggcc ctggaccac cacac caaat ggagctgact cagtgaacac tgggaattaaa 4080
aggaaagtca agaagaatga actatgtcga tgcacagtat cttttctttc aaaagtagag 4140
caaaactata ggttttggtt ccacaatctc tacgactaat cacctactca atgcctggag 4200
acagatacgt agttgtgctt ttgtttgctc ttttaagcag tctcactgca gtottatttc 4260
caagtaagag tactgggaga atcactaggt aacttattag aaacccaaat tgggacaaca 4320
gtgctttgta aattgtgttg tcttcagcag tcaatacaaa tagatttttg tttttgttgt 4380
tctgcagcc ccagaagaaa ttaggggtta aagcagacag tcacactggt ttggtcagtt 4440
acaaagtaat ttctttgatc tggacagaac atttatatc a gtttcatgaa atgattggaa 4500
tattacaata ccgttaagat acagtgtagg catttaactc ctcatggcg tgggtccatgc 4560
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aaatattaca caggaggcct tcggagtttc ttagtcatta ctgtcctttt cccctacaga 4740
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aaaatcacca aaaacat

```

4877

<210> 201
 <211> 153
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(153)
 <223> 3' terminal sequence. hmt1 (hnrnp
 methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
 gene.

```

<400> 201
attagacctc acattaggga aaacatcaaa atgantcacg cagcaccctt gagatcctga 60
ggttggccca gccgagcccg tgctcagaag cccccagct cgggccccca gctgcccga 120
cgcccgcct caccagcagg caggtoccca tcc

```

153

<210> 202
 <211> 472
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(472)
 <223> 5' terminal sequence. hmt1 (hnrnp
 methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)
 gene.

```

<400> 202
agtgaatcgc agggagaaga gcctgctgag tncagtgagg cgggtctcct gcaggaggga 60
gtacagccag aggagtttgt ggccatcgcg gactacgtg ccacgatga gaccagctc 120
agttttttga gaggagaaaa aattcttatc ctgagacaaa cactgcaga ttggtggtgg 180
ggtgagcgtg cgggctgctg tgggtacatt c cggcaaac atgtggggaa gcacgtgat 240
gagtacgacc ccaggacac gtggcaggat gaagagtact tcggcagcta tggaaactctg 300

```

132/292

```

aaactccact tgggagatgt tggcagacca gccacgaaca actaaatacc acagtgttca 360
ttctctgnac gaattaaaga atccctgnac ggnttaaagt tcttcnnggg acgtggggct 420
gtgggggattt gggatccntc agtctcttnt tgttgacacat tttgcgtggc nt 472

```

<210> 203

<211> 2093

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2093)

<223> hmt1 (hmrnp methyltransferase, s.
cerevisiae)-like 1 (HRMT1L1) gene.

<400> 203

```

cactgcgctt gcgcgggttg agggcgggtg ctcagtctcc tggaaaggac cgtccacccc 60
tccgcgctgg cgggtgtggac gcggaactca gcggagaaac gcgattgaga aatggaaaag 120
aaaatgaaat aaatcagcag ttatgaggca gagcctaaga gaactatggc aa catcaggt 180
gactgtccca gaagtgaatc gcagggagaa gagcctgctg agtgacgtga ggcgggtctc 240
ctgcaggagg gagtacagcc agaggagttt gtggccatcg cggactacgc tgccaccgat 300
gagaccagc tcagtttttt gagaggagaa aaaattctta tcctgagaca aaccactgca 360
gattggtggt ggggtgagcg tgcgggctgc tgtgggtaca ttccggcaaa ccatgtgggg 420
aagcacgtgg atgagtaaga ccccgaggac acgtggcagg atgaagagta cttcggcagc 480
tatggaactc tgaactcca cttggagatg ttggcagacc agccacgaac aactaaatac 540
cacagtgtca tcctgcagaa taaagaatcc ctgacggata aagtcacctt ggacgtgggc 600
tgtgggactg ggatcatcag tctcttctgt gcacactatg cgcggcctag agcgggtgtac 660
gcggtggagg ccagtggagt gcacagcac acggggcagc tggctcctgca gaacggcttt 720
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agtgtgtccc ttactgcctg cgtcctacca ctgctgtggg acgtaggatt gcaca gggct 1920
gtgccagtgg cgtgtaggga aactgcctt ggctcagcgt gcgagctaag gtggcgatgt 1980
atgcgatggg actctgcatg ggatagtaca gttgtgtaga cgtcttccaa ataaattatg 2040
tgttggtgcc atcgacatg ctcaataaat attttaaat agtgaaaaaa aaa 2093

```

<210> 204

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 204

```
tgggggcctt tatta aggtc tggcagatgt ggtggaggtg gaagtacaaa cccaggcctg 60
ggcctaggaa agggcagaag aaaggcaaag ggtcccttgg agcaggaacc catccctctc 120
tgcttatacc cagcaccctt catcccaggt tcctttcttc aacctccgcc tgctcttggg 180
aacacagagc accaagaact gacaaaccgg gaccctccag gggccacagc gtgggggc ag 240
agtccagggn ttctgtctcc ccgcagtggg gagatctngg ggagctcagg tgaacctcct 300
cancctcctg ccagtatgaa gttggggaag cgccttttct tgtccccag aacagaacaa 360
actcttgttc tctgtgggtt ngggggaaaa ggtttngggg ggtttggact taggggagaa 420
gttnagcttg a                                     431
```

<210> 205

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. ets variant gene 4
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 205

```
gtccccctgcc cctgcccttg gacagtcgcc cctacagncc tttccccggg cagagaacgg 60
aatttcctga gatcctcttg cacctcccag cccaccctg gccatgggta cctcggggaa 120
catagctccg tcttcacga gcccctggga catttgccac tccttcacat ctcagggagg 180
gggccgggaa cccctcccag gcccctacc aacaccagct gtccgagccc tgcccaccct 240
atccccagca gagctttaag caagaatacc atgatcccct gtatggaaca gggnggggcc 300
agccaggccg tgggaaccag ggtgggggt tcaatggggg cacagggtac ccaggggggn 360
ggggggttg ttgattcaaa acagggaaca gacgggattt tt ggnttaag gatttnaggt 420
tntttaancg ggttg                                     435
```

<210> 206

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(447)

<223> 5' terminal sequence. annexin a11 (ANXA11)
gene.

<400> 206

134/292

```

agacccagct cctctttgac atttatgaga taaaggaagc catcaagggg gttggcactg 60
atgaagcctg cctgattgag atcctcgctt cccgcagcaa tgagcacatc cgagaattaa 120
acagagccta caaagcagaa ttcaaaaaga ccctggaaga ggcca ttoga agcgacacat 180
cagggcactt ccagcggctc ctcatctctc tctctcaggg aaaccgtgat gaaagcacia 240
acgtggacat gtactcgcc cagagagatg cccaggagc tgtatgcggn ccggggagaa 300
ccgcctgggg aacagacgag tccaagtttc aattgcggtt tctgtggctt cccgggagcc 360
gggcncacc tgggtaggca gtt tttcaat gagttaccag agaatgnaca gggcncggac 420
attnntagaa gacatctgc ccggaga 447

```

<210> 207

<211> 1958

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1958)

<223> annexin all (ANXA11) gene.

<400> 207

```

gctgctgcgc ccgcggtctc ccagtgcctc gagtgccccg cgggccccgc gagcgggagt 60
gggacccagc cctaggcaga acccaggcgc cgcgcgccgg acgcccgcgg agagagccac 120
tcccgcacac gtccatttcc gcccctcgcg tccggagtcc ccgtggc cag atctaaccat 180
gagctaccct ggctatcccc cgcctccagg tggtaccaca ccagctgcac caggtggtgg 240
tccctgggga ggtgctgect accctcctcc gcccgcatg ccccccacg ggctggataa 300
cgtggccacc tatcgggggc agttcaacca ggactatctc tcgggaatgg cggccaacat 360
gtctgggaca ttggaggag ccaac atgcc caacctgtac cctggggccc ctggggctgg 420
ctaccacca gtgcccctg gcggttttgg gcagccccc tctgccagc agcctgttcc 480
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gccataccca ggggcccctg tgccgggcca gcccatgcca ccccccggac agcagcccc 600
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tgggcagcag cagccagtgc cagactaccc aggatacccc ggggtctggga ctgtcaccoc 720
cgctgtgccc ccaaccagct ttggaagccg aggcaccatc actgatgctc ccggctttga 780
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caaggccatg aggggggcag gaacaaagga ccggaccctg attcgcatca tgggtgtctc 1560
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gtaccacgac atctcgggag atacttcagg ggattaccgg aagattctgc tgaagatctg 1680
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gtgccaggaa aaggccaaaa gaatgtctgt ttctaacaaa tccacaaata gccccgagat 1800
tcacctctct agagcttagg cctgtcttcc acccctcctg acccgatatg tgtgccacag 1860
gacctgggct ggctagaac tctctcagga tgccttttct accccatccc tcacagcctc 1920
ttgctgctaa aatagatggt tcatTTTTCT gaaaaaaa 1958

```

<210> 208

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 5' terminal sequence. platelet-derived
growth factor receptor, beta polypeptide (PDGFRB)
gene.

<400> 208

```
gccagatgaa gcaaggccat ataccctaaa cttccatcct gggggtcagc tnggctcctg 60
ggagattcca gatcacacat cacactctgg ggactcagga accatgcccc ttccccaggc 120
ccccagcaag tctcaagaac acagctgcac aggccttgac ttagagtnac agccggntnc 180
ctggaagcc cccagcagct gccccaggga catgggaaga ccacgggacc tctttcacta 240
cccacgatga cctccggggg tatcctgggg caaaagggac aaagagggca aatgagatca 300
cctnctgcag cccaccactt ccagcactg tgccgaggtt ttic gttcga agacagaatt 360
ggacagttag ggacagttat tgtctttntt taaaagnaca aggaaggttt cagnttgggt 420
taccaccaag gag                                     433
```

<210> 209

<211> 5570

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5570)

<223> platelet-derived growth factor receptor,
beta polypeptide (PDGFRB) gene.

<400> 209

```
ggccctcag cctgtctgcc cagcacgagc ctgtgtctgc cctgcccaac gcagacagcc 60
agaccaggg cgccctctct ggcggtcttg ctctcccgga aggatgcttg gggagtgagg 120
cgaagtggg cgctctcttc ccctacagca gcccccttc tccatccctc tgttctcctg 180
agccttcagg agcctgcacc agtctgcct gtcttctac tcagtgtta cccactctgg 240
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tgttacttct ggaaccacag atctctcagg gcctggctgt cacaccccg gggccagagc 480
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ccagcgtgct cacactgacc aacctcactg ggctagacac gggagaatac ttttgacccc 660
acaatgactc ccgtggactg gagaccgatg agcggaaacg gctctacatc tttgtgccag 720
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```

tgggcacact acaatttggct gagctgcacg ggagccggac actgcaggta gtgttcgagg 1380
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 cttgacttag agtgacagcc ggtgtcctgg aaagccccaa gcagctgcc cagggacatg 4920
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137/292

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gggacaaaga gggcaaatga gatcacctcc tgcagcccac cactccagca cctgtgccga 5040
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ttacaaatat ttttaggact cacgttaact cacattata ca gcagaaat gctattttgt 5520
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<210> 210

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 5' terminal sequence. williams-beuren
syndrome chromosome region 14 (WBSCR14) gene.

<400> 210

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gaccggcgta tcacacacat ctccgcgga caggagcggc gcttcaacat caagctgggg 60
tttgacaccc ttcatgggct cgtgagcaca ctcaagtccc agcccagcct caaggtgagc 120
aaagctacca cgctgcagaa gacagctgag tacatcctta tgctacagca ggagcgtgcg 180
ggcttgcaag aggaggccca gcagctgcgg ggatgagatt gaggagctca atgccgccat 240
taacctgtgc cagcagcagc tgcccgccac aggggtaccc attcacacac cagcgttttg 300
accagatgcg agacatgttt gatggactac gtccgaaccc gtacgctgca caa ctgggaa 360
gttctggggg ntctcagcat cctnattccg gcctctgttt tgagtc 406

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<210> 211

<211> 3293

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3293)

<223> williams-beuren syndrome chromosome region
14 (WBSCR14) gene.

<400> 211

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ccccgcgctg cgcggagcag ggaccaggcg gttgcggcgg cgacagccat ggccggcgcg 60
ctggcaggtc tggccgcggg cttgcaggtc ccgcgggtcg cggccagccc agactcggac 120
tcggacacag actcggagga cccaggtctc cggcgcagc g cgggcgggctt gctccgctcg 180
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cggcgcgacc aggaggggtc cgtggggccc tccgacttcg ggccgcgcag tatcgacccc 300
aactcacac gcctcttcga gtgcttgagc ctggcctaca gtggcaagct ggtgtotccc 360
aagtgaaga atttcaa agg cctcaagctg ctctgcagag acaagatccg cctgaacaac 420
gccatctgga gggcctggta tatccagtat gtgaagcgga ggaagagccc cgtgtgtggc 480
ttcgtgaccc ccctgcaggg gcctgaggct gatgcgcacc ggaagccgga ggccgtggtc 540
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cgcctctact acaagaagcg gctccgtaag cccagcaggg aagatgacct cctggccctt 660
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agcagggcag gcacatg tg tgtgtgtgtg tgtggatgtg tgtgtgtggg tttgtaaaag 3240
aattcttgac caataaaagc aaaaactgtc tgctggttaa aaaaaaaaaaaa 3293

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<210> 212

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(207)

<223> 5' terminal sequence. cd74 antigen

(invariant polypeptide of major histocompatibility
complex, class ii antigen-associated) (CD74) gene.

<400> 212
ccttttgccct tggcttttct agtcctatct acctgtcagg ctgagccatc tctcttccc t 60
ttccccagtc atcactcccc aaggaagagc caatgttttc cacccataat cttttctgcc 120
gaccctagt tccctctgct cagccaagct tgttatcagc tttcagggcc atngttcaca 180
ttagaataaa aggtagtaat taganaa 207

<210> 213
<211> 1304
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1304)
<223> cd74 antigen (invariant polypeptide of major
histocompatibility complex, class ii
antigen-associated) (CD74) gene.

<400> 213
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tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctgggccc ggcgccctgg 120
ggccccggag agcaagtga gcccgggagc cctgtacaca ggcttttcca tcctgggtgac 180
tctgtctctc gctggccagg ccaccaccgc ct acttcctg taccagcagc agggccggct 240
ggacaaaactg acagtacact cccagaacct gcagctggag aacctgcgca tgaagcttcc 300
caagcctccc aagcctgtga gcaagatgcg catggccacc ccgtgtctga tgcaggcgct 360
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gaaggtcttt gagagctgga tgcaccattg gctcctgttt gaaatgagca ggcactcctt 600
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gtcttcaaca tcctgccagc cccacacagc tacagctttc ttgtccctt cagccccag 780
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tgcccaatct ccattctgtc acagggggcgt gaggtcccag gaagtggcca aaagctagac 960
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ggaccataa tcctttctgc cgaccctag ttccctctgc tcagccaagc ttgttatcag 1260
ctttcagggc catggttcac attagaataa aaggtagtaa ttag 1304

<210> 214
<211> 355
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(355)
<223> 5' terminal sequence. annexin a7 (ANXA7)
gene.

<400> 214

aggaactatc cgaccagctg ccaacttcga tgctataaga gatgcagaaa ttcttcgtaa 60
ggcaatgaag ggttttggga cagatgagca ggcaattgtn gatgtngttg ccaaccgttt 120
ccaatgatca gaggcaaaaa attaaagcag catttaagac ctctatggc aaggatttaa 180
tcaaagatct caaatcagag ttaagtngaa atatggaaga actgatcctn ggccctcttc 240
atgcctccta cgtattacga tgctngagc ttacggaaa gcaatncagg gancaggta 300
tcaggancgt tgtatttgat ttgngatfff ngtgcacang atcanattca ggtaa 355

<210> 215

<211> 2176

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2176)

<223> annexin a7 (ANXA7) gene.

<400> 215

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atgtcatacc caggctatcc cccaacaggc taccacctt tccctggata tccctctgca 120
ggtcaggagt catcttttcc cccttctggt cagtatcctt atcctagtgg ctttccctca 180
atgggaggag gtgcctaccc acaagtgcc ahtagtggt acccaggagc tggaggctac 240
cctggcctg gaggttatcc agcccctgga ggctatcctg gtgcccaca gccaggggga 300
gctccatcct atcccggagt tctccaggc caaggattg gagtcccacc agg tggagca 360
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ccactacctg gtggttttcc tggaggacag atgccttctc agtatcctgg aggacaacct 480
acttacccta gtcagatcaa tacagattct ttttcttctc atcctgtttt ctctcctgtt 540
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ataaaaaatt gcatat 2176

<210> 216
<211> 525
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(525)
<223> 3' terminal sequence. thrombospondin 1
(THBS1) gene.

<400> 216
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attcaggagt gtgacaagag atttaaacag gatggtggct ggagcntgng ttccccgtgg 120
tcatcttggt ctgtgacatg tggatggtgt gtgatcacia ggatccggct ctgcaactct 180
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tctttttaat tgaaaaacaa attcacntt ttccccagct ttttttcctt gtgttcaggg 480
gaggcagagg ttttttgaac ggnnttaggg gatttttgnc aagtt 525

<210> 217
<211> 5722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5722)
<223> thrombospondin 1 (THBS1) gene.

<400> 217
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cgccgcgctc cgttacacac aggatccctg ctgggcacca acagctccac catggggctg 120
gcctggggac taggcgtcct gttcctgatg catgtgtgtg gcaccaaccg cattccagag 180
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143/292

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```

<210> 218

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(397)

<223> 3' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 218

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ttaatgctgc caaaaagtat aaaaatacag taggaatggc agtacaatac aaagtaatct 60
ctcctaattt atttcttgta catctttcta catttcatac actcattaaa aacacttaac 120
acatccaatt aaaggttctg caaagtcttc tgctgggtgg tgctcttcat cccctgggnt 180
gtaaagttta ctttgtaaac aaacaactgt gaggncaatc tagagggtta ggcgagcctc 240
actttagttt ccggagtggg gcttcagggt cttgctttgc acatcaatgg gttcaaaatt 300
tataggctgc aggaatatc tcaaggatcat ggaatattag ggngtctggt ncaat cttgg 360
ggcccttttt tcttttttcg ttncatttct ccattta 397

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<210> 219

<211> 338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(338)

<223> 5' terminal sequence. protein tyrosine
phosphatase, non-receptor type 2 (PTPN2) gene.

<400> 219

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ggctccttga accctgacca tgggcctgcg gtgatccact gtagtcagg cattgggcgc 60
tctggcacct tctctctggt agacacttgt cttgttttga tggaaaaagg agatgatatt 120
aacataaaac aagtgttact gaac atgaga aaatacogaa tgggtcttat tcagacccca 180
gatcaactga gattctcata catggctata atagaaggag caaatgtat aaaggagat 240

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tctagtatac agaaacgatg gaaagaactt tctaaggang acttatctcc tgcctttgat 300
cattncacca aacaaaataa tgactgaaaa atacantg 338

<210> 220

<211> 2287

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2287)

<223> protein tyrosine phosphatase, non -receptor
type 2 (PTPN2) gene.

<400> 220

ggggggcctg agcctctccg ccggcgcagg ctctgctcgc gccagctcgc tcccgcagcc 60
atgcccacca ccatcgagcg ggagttcgaa gaggttgata ctacagctcg ctggcagccg 120
ctgtacttgg aaattcgaaa tgagtcccat gactatcctc atagagtggc caagtttcca 180
gaaaacagaa atcgaaacag atacagagat gtaagcccat atgatcacag tctgtgttaa 240
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gtttggcagc agaagaccaa agcagttgtc atgctgaacc gcattgtgga gaaagaatcg 420
gttaaatgtg cacagtactg gccaacag at gaccaagaga tgctgtttaa agaaacagga 480
ttcagttgta agctcttctg agaagatgtg aagctgtatt atacagtaca tctactacaa 540
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tccatttttc taaaaagaag tttgatatga gcagttagaa gttggaataa g caatttcta 1980
ctatatattg catttctttt atgttttaca gttttcccca ttttaaaaag aaaagcaaac 2040
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tcaggtaaac agttggtcaa gactttgtaa agaaattggg ttctgtaaat cccattattg 2160
atatgtttat ttttcatgaa aatttc aatg tagttggggg agattatgat ttaggaagca 2220
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taaacc 2287

<210> 221

<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(296)
<223> 3' terminal sequence. epha2 (EPHA2) gene.

<400> 221
ctcggctggc tcacacaccc gtatggcaaa ggggtgggacc tgatgcagaa catcatgaat 60
gacatgccga tctacatgta ctccgtgtgc aacgtgatg t ctggcgacca gganaactgg 120
ctccgcacca actgggtgta ccgaggagag gctgagcgta tcttcattga gctcaagttt 180
actgtacgtg actgcaacag cttccctggg tggcgccant tcttggaag gagactttca 240
accttacta tgccgagtcg gacctgggac tacggcanca acttncagaa ggcgct 296

<210> 222
<211> 3921
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3921)
<223> epha2 (EPHA2) gene.

<400> 222
cggaagtgtg gcgcaggccg gcggggcgga gcggacaccg aggcgcgcgt gcaggcgtgc 60
gggtgtgcgg gagccgggct cggggggatc ggaccgagag cgagaagcgc ggcattggagc 120
tccaggcagc ccgcgcctgc ttcgccctgc tgtggggctg tgcgctggcc gcggccgcgg 180
cggcgagagg caaggaagtg gtactgtctg actttgtctg agctggaggg gagctcggct 240
ggctcacaca ccggtatggc aaaggggtggg acctgatgca gaacatc atg aatgacatgc 300
cgatctacat gtactccgtg tgcaacgtga tgtctggcga ccaggacaac tggtcccgca 360
ccaactgggt gtaccgagga gaggctgagc gtaacaactt tgagctcaac tttactgtac 420
gtgactgcaa cagcttcctt ggtggcgcca gctcctgcaa ggagactttc aacctctact 480
atgccgagtc ggacctggac tacgg cacca acttccagaa gcgcctgttc accaagattg 540
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atgtgcgccg caccgaggggt ttctccgtga ccct ggacga cctggccccca gacaccacct 1620

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agttgcagat gattcaaac g 3921

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<210> 223

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 3' terminal sequence. tissue inhibitor of
 metalloproteinase 1 (erythroid potentiating
 activity, collagenase inhibitor) (TIMP1) gene.

<400> 223

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ggaacagggt ggacactgtg caggcttcag ctccactcc gggcaggatt caggctatct 60
gggaccgcag gacttgccag gngcacagcc ctggctccc aggcaggcag gcaaggtgac 120
gggactggaa gcccttttca nacccttga ggagctggnc cgtccacaag caatgagtgc 180
cactctgcag tttgcagggg atggataaac agggaaacac tgtgcattcc tcacagccaa 240

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cagtntaggt cttggtnaag ccccgcgct gagctaagct caggcttttc caggggagcc 300
acgaaactnc aggtagtgat gtgcaagagt ccatcctgca gttttccagc aatnagaaac 360
tcctcgttng cggtttttgg ggaccnttgg aagtnttc cg cagacatttt tccatgggcc 420
gggttttaag acgaacc 437

<210> 224

<211> 466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(466)

<223> 5' terminal sequence. tissue inhibitor of
metalloproteinase 1 (erythroid potentiating
activity, collagenase inhibitor) (TIMP1) gene.

<400> 224

gccncagatc cagcgccag agagacacca gagaaccac catggccccc tttgnagccc 60
ctggcttctg gcatectgtt g ttgctgtgg ctgatagccc ccagcagggc ctgcacctgt 120
gtcccacccc acccacagac ggccttctgc aattccgacc tcgtcatcag ggccaagtgc 180
gtggggacac cagaagtcaa ccagaccacc ttataccagc gttatgagat caagatgacc 240
aagatgtata aagggttcca agccttaggg gatgccgctg acatccggtt cgtctacacc 300
cccgccatgg agagtgtctg cggatacttn cacagggtccc acaaccgnag cgaggagttt 360
ctcattngct ggaaaactgt aggatggact tcttgacat tnactacctt gcagttttng 420
tgggttcctt gggaacagtc tgaggtttag tttagcggtt ggggtt 466

<210> 225

<211> 782

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(782)

<223> tissue inhibitor of metalloproteinase 1
(erythroid potentiating activity, collagenase
inhibitor) (TIMP1) gene.

<400> 225

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ccatggcccc ctttgagccc ctggcttctg gcatectgtt gttgctgtgg ctgatagccc 120
ccagcagggc ctgcacctgt gtcccacccc acccacagac ggccttctgc aattccgacc 180
tcgtcatcag ggccaagtgc gtggggacac cagaagtcaa c cagaccacc ttataccagc 240
gttatgagat caagatgacc aagatgtata aagggttcca agccttaggg gatgccgctg 300
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acaaccgcag cgaggagttt ctcattgctg gaaaactgca ggatggactc ttgcacatca 420
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agtccctgcg gtcccagata gcctgaatcc tgcctcgga ggaactgaag cctgcacagt 720
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gc

782

<210> 226
 <211> 353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(353)
 <223> 5' terminal sequence. ephrin -a1 (EFNA1)
 gene.

<400> 226
 acagctacta ctacatctca gccaaaccca tccaccagca tgaagaccgc tgcttgaggt 60
 tgaaggtgac tgtcagtggc aaaatcactc acagtcctca ggcccatgtc aatccacagg 120
 agaagagact tgcagcagat gaccagagg tgccgggttct acatagcatc ggtcacagtg 180
 ctgccccacg cctcttccca cttgcctgga ctgtgctgct ccttcactt ctgctgctgc 240
 aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag ggaca ggctg aagagaggga 300
 caggcactcc aaacctgtct tgggggccac ttccagagcc cccagccctt ggg 353

<210> 227
 <211> 1480
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(1480)
 <223> ephrin-a1 (EFNA1) gene.

<400> 227
 gcggagaaag ccagtgggaa cccagaccca taggagaccc ggcgtcccgcc tcggcctggc 60
 caggcccccgc gctatggagt tcctctgggc ccctctcttg ggtctgtgct gcagtctggc 120
 cgctgtgtat cgccacaccg tcttctggaa cagttcaaatt cccaagttcc ggaatgagga 180
 ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240
 tcaactctgtg gcagacgctg ccatggagca gtacatactg tacctggtgg agcatgagga 300
 gtaccagctg tgccagcccc agtccaagga ccaagtcgcg tggcagtgc accggcccag 360
 tgccaagcat ggcccggaga agctgtctga gaagttccag cgcttcacac ctttcaccct 420
 gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480
 tgaagaccgc tgcttgaggt tgaaggtgac tgtcagtggc aaaatcactc acagtcctca 540
 ggcccatgtc aatccacagg agaagagact tgcagcagat gaccagagg tgccgggttct 600
 acatagcatc ggtcacagtg ctgccccg cctcttccca cttgcctgga ctgtgctgct 660
 ccttcactt ctgctgctgc aaaccccggtg aaggtgtatg ccacacctgg ccttaaagag 720
 ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttccagagccc 780
 ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaaacgg 840
 gtcagtatta aggttttcaa ccggaaggag gccaaaccagc ccgacagtgc catccccacc 900
 ttacactcgg agggacggag aaagaagtgg agacagtcct tccccaccat tctgccttt 960
 aagccaaaga aacaagctgt gcaggcatgg tcccttaagg cacagtggga gctgagctgg 1020
 aagggggccac gtggatgggc aaagcttgtc aaagatgccc cctccag gag agagccagga 1080
 tgcccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140
 caggagaggc agcatgcttg ggctgacca gcatctccca gcaagacctc atctgtggag 1200
 ctgccacaga gaagtttcta gccaggctact gcattctctc ccatcctggg gcagcactcc 1260

149/292

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ccagagctgt gccagcaggg g ggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgtccatg tgtacattct gcctagagt tagcctaaag ggcagggccc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaat aaagcaatgt gttttttcgg 1480

```

<210> 228

<211> 170

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(170)

<223> 3' terminal sequence. endothelin receptor
type a (EDNRA) gene.

<400> 228

```

ttttaagggt tctgtaaact tttattttac acttatgggc cactgcaact cagggccttg 60
gcttctggct catttctaca aagttacttg ttgaaaagat gtagtaaagg tagaaattgg 120
aaatatcct gctagtaaac cacagttact taccagtcca taaataaaat 170

```

<210> 229

<211> 4105

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4105)

<223> endothelin receptor type a (EDNRA) gene.

<400> 229

```

gaattcgcg g cgcctcttg cgggtcccaga gtggagtgga aggtctggag ctttgggagg 60
agacggggag gacagactg g aggcgtgttc ctccggagtt ttctttttcg tgcgagccct 120
cgcgcgcgcg tacagtcac cgcgtgttct gacgattgtg gagaggcggg ggagaggcctt 180
catccatccc acccggtcgt cgccggggat tggggtccca gcgacacctc cccgggagaa 240
gcagtgccca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgccgcgc 300
cgagccccgg gacaccggcc accctccgcg ccaccacccc tcgctttctc cggcttctc 360
tgccccaggg gccgcgcgga cccggcagct gtctgcgcac gccgagctcc acggtgaaaa 420
aaaaagtga ggtgtaaaag cagcacaagt gcaataagag atatttcctc aaatttgcc 480
caagatgaa accctttgcc tcagggcac cttttggct g gcactgggtg gatgtgtaat 540
cagtataat cctgagagat acagcacaat tctaagcaat catgtggatg atttcaccac 600
ttttcgtggc acagagctca gcttcttggt taccactcat caaccacta atttggtcct 660
accagcaat ggtcaatgc acaactattg ccacagcag actaaaatta cttcagcttt 720
caaatatatt aacactg tga tatctgtac tattttcatc gtgggaatgg tggggaatgc 780
aactctgtc aggatcattt accagaacaa atgtatgagg aatggcccca acgcgtgat 840
agccagtctt gcccttgagg acqttatcta tgttggtcatt gatctcccta tcaatgtatt 900
taagctgctg gctgggcgct ggccttttga tcacaatgac tttggcgat ttctttgca a 960
gtgtttcccc tttttgcaga agtcctcggt ggggatcacc gtcctcaacc tctgcgtct 1020
tagtggtgac aggtacagag cagttgcctc ctggagtcgt gttcagggaa ttgggattcc 1080
tttggttaact gccattgaaa ttgtctccat ctggatcctg tcctttatcc tggccattcc 1140
tgaagcgatt ggcttcgtca tgggtaccct tgaa tatagg ggtgaacagc ataaaacctg 1200
tatgctcaat gccacatcaa aattcatgga gttctaccaa gatgtaaagg actggtggct 1260

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cttcgggttc tattttotgta tgcccttggt gtgcactgcg atcttctaca cctcatgac 1320
ttgtgagatg ttgaacagaa ggaatggcag cttgagaatt gccctcagtg aacatcttaa 1380
gcagcgtoga gaagtggcaa aaacagtttt ctgcttggtt gtaatttttg ctctttgctg 1440
gttccctctt cacttaagcc gtatattgaa gaaaactgtg tataacgaaa tggacaagaa 1500
ccgatgtgaa ttacttagtt tcttactgct catggattac atcgggtatta acttggcaac 1560
catgaattca tgtataaac ccatagtctt gtattttgtg agcaagaa at ttaaaaattg 1620
tttccagtca tgcctctgct gctgctgtta ccagtcctaaa agtctgatga cctcgggtccc 1680
catgaacgga acaagcatcc agtggaagaa ccacgatcaa aacaaccaca acacagaccg 1740
gagcagccat aaggacagca tgaactgacc acccttagaa gcactcctcg gtactcccat 1800
aatcctctcg gagaaaaaaa tc acaaggca actgtgactc cggaatctc ttctctgatc 1860
cttcttctct aattcactcc cacacccaag aagaaatgct ttccaaaacc gcaaggtaga 1920
ctggtttatc caccacaac atctacgaat cgtacttctt taattgatct aatttacata 1980
ttctgcgtgt tgaattcagc actaaaaaat ggtgggagct gggggagaat gaagactgtt 2 040
aaatgaaacc agaaggatat ttactacttt tgcattgaaa tagagcttc aagtacatgg 2100
ctagctttta tggcagttct ggtgaatggt caatgggaac tggtcacat gaaactttag 2160
agattaacga caagattttt tacttttttt aagtgtttt ttgtccttca gccaaacaca 2220
atatgggctc aggtcacttt tatttgaaat gtcatt tggg gccagtattt ttaactgca 2280
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aatagtatc aggtgagcaa ttagattagt attttccacg tcaactattta tttttttaa 2400
acacaaatc taaagctaca acaataacta caggccctta aagcacagtc tgatgacaca 2460
tttggcagtt taatagatgt tactcaaaga attttttaag aactgtattt tttttttaa 2520
atggtgtttt attacaagg accttgaaca tgttttgtat gttaaattca aaagtaatgc 2580
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atgattccga aattttcatt caggatattg taatagtgc atatatatgt atatacatat 2820
cacctcctat tctcttaatt ttgttaaaa tgttaactgg cagtaagtct tttttgatca 2880
ttcccttttc catataggaa acat aatttt gaagtggcca gatgagtta tcatgtcagt 2940
gaaaaataat taccacaaa tgccaccagt aacttaacga ttcttactt cttggggttt 3000
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gtctgagcta aaatctaggt gattgttcat catgacaa cc tgcctcagtc cattttaacc 3360
tgtagcaacc ttctgcattc ataaatcttg taatcatgtt accattacaa atgggatata 3420
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tggtttgata aagcagttat tggggtcata ttgtttcctg tgctggagca aaagtcatta 3540
cactttgaag tattatattg ttcttactc caattcaatg tggatgatga attgccaggt 3600
tgtctgatat ttctttcaga cttcgccaga cagattgtcg ataataaatt aggtgaagata 3660
atttgttggg ccatatttta ggacaggtaa aataacatca ggttccagtt gcttgaattg 3720
caaggctaag aagtactgcc cttttgtgtg ttagcagtc aatctattat t ccaactggcg 3780
catcatatgc agtgatatat gcctataata taagccatag gttcacacca tttgttttag 3840
acaattgtct ttttttcaag atgctttgtt tctttcatat gaaaaaaatg cattttataa 3900
attcagaaag tcatagattt ctgaaggcgt caacgtgcat tttatttatg gactggtaag 3960
taactgttgt ttactagcag gaatat ttcc aattttctacc ttactacat cttttcaaca 4020
agtaactttg tagaaatgag ccagaagcca aggcctgag ttggcagtg ccataagtg 4080
taaaataaaa gtttacagaa acctt 4105

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<210> 230

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 230

ggtttcttgt tttttattat tggcgtcagt agngactata cgtggcctta aacgtcatgc 60
actgatggac agaagagaaa aaaggatgaa aaaaaagaca aaggagggga aagaggagca 120
gcagtgaan tttgtaataa aaactcttct taatttatag gtaagttttg gcatttttaa 180
atccaacgcc cctcccacc cctaaaagt ccaaccaaag tgagagggtc acagggtgac 240

<210> 231

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(475)

<223> 5' terminal sequence. growth factor
receptor-bound protein 2 (GRB2) gene.

<400> 231

cttaatggaa aagacggctt cattcccaag aactacatag aaatga aacc acatccgtgg 60
ttttttggca aaatccccag agccaaggca gaagaaatgc ttagcaaaca gcggcacgat 120
ggggcctttc ttatccgaga gagtggagagc gctcctgggg acttctccct ctctgtcaag 180
tttggaaacg atgtgcagca cttcaagggtg ctccgagatg gagccgggaa gtacttcctc 240
tgggtggtga agttcaattc ttgga atgag ctggtggatt atcacagatc tacatctgtc 300
tccagaaacc agcagatatt cctgcgggga cattaggaac aggtgccaca gcaggccgac 360
atacgttoca ggggcctttt tttgattttt gattccccag gggggnttgg ngagggtggg 420
ttttccgccg ggggagattt tattccatgt tcntgggttn aatttaggaa ccntt 475

<210> 232

<211> 1109

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1109)

<223> growth factor receptor-bound protein 2
(GRB2) gene.

<400> 232

gccagtgaat tcgggggctc agccctcctc cctcccttcc ccctgcttca ggctgctgag 60
cactgagcag cgctcagaat ggaagccatc gccaaatatg acttcaaagc tactgcagac 120
gacgagctga gttcaaaaag gggggacatc ctcaagggtt tgaacgaaga atgtgatcag 180
aactggtaca aggcagagct taatggaaaa gacggcttca ttccaagaa ctacatagaa 2 40
atgaaaccac atccgtggtt ttttgcaaaa atccccagag ccaaggcaga agaaatgctt 300
agcaaacagc ggcacgatgg ggcctttctt atccgagaga gtgagagcgc tcctggggac 360
ttctccctct ctgtcaagtt tggaaacgat gtgcagcact tcaagggtgct ccgagatgga 420
gccgggaagt acttctctg ggtggtgaag ttcaattctt tgaatgagct ggtggattat 480
cacagatcta catctgtctc cagaaaccag cagatatctc tgcgggacat agaacagggtg 540
ccacagcagc cgacatacgt ccaggccctc tttgactttg atccccagga ggatggagag 600
ctgggcttcc gccggggaga ttttatccat gtcatggata actcagaccc caactggtgg 660

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aaaggagctt gccacggg ca gaccggcatg tttccccgca attatgtcac ccccgatgaac 720
cggaacgtct aagagtcaag aagcaattat ttaaagaaag tgaaaaatgt aaaacacata 780
caaaagaatt aaaccacaa gctgcctctg acagcagcct gtgagggagt gcagaacacc 840
tggccgggtc accctgtgac cctctcactt tgggttggaac tttagggggg gggagggggc 900
gttgatttta aaaaagccaa aacttaccta taaattaaga agagttttta ttacaaattt 960
tactgtctgc tctcttttcc cctcctttgt cttttttttc atcctttttt ctcttctgtc 1020
catcagtgcg tgacgtttta ggccacgtat agtcctagct gacgccaata ataaaaaaca 1080
agaaacaaaa aaaaaaaaaa ccgaattca 1109
```

<210> 233

<211> 446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(446)

<223> 3' terminal sequence. jun d proto -oncogene
(JUND) gene.

<400> 233

```
cgcgctctc ggctgccnng ntgtacaccg cgccggaaag tggggctccg agggggcgca 60
ctcaaaaccc tgccttttct tttttttttt ttttctttgg aagagagaag 120
aacagagtgt tcgattctgc cctatttatg tttctactcg ggaacaaacg ttggttgtgt 180
gtgtgtgtgt tttcttgtgt tgggttttta a agaaatggg aagaagaaaa aaaaattctc 240
cgcccccttc ctgatctcgc ctcccccttc cggttctttc gaccgggtcc cccctccctt 300
tttttgttct gttttgtttt gttttgctac gagtcacat tctgtttgt aatccttggg 360
ttcgnccggt tttctgtttt cagtaaagtc tcgttacggc aaaacctcgt gccgaatttt 420
tggggctcga ggggcaaaat ttccca 446
```

<210> 234

<211> 1891

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1891)

<223> jun d proto -oncogene (JUND) gene.

<400> 234

```
ccgaggttat aagaggggcg acaagtggcg cgccgcagga gccgccgcca gtggaggggc 60
gggcgctgcg gccgcggccg gggcgggcg agggccgagc ggacgggggg gcgcggggcc 120
cccgaggagg cgccggcact cccccccggg ccggcgcggc gggggaggcg gaggatggaa 180
acacccttct acggcgatga ggcgctg agc ggcctgggcg gcggcgccag tggcagcggc 240
ggcacgttcg cgtccccggg ccgcttggtc ccggggggcg ccccgacggc cgcggccggc 300
agcatgatga agaaggacgc gctgacgctg agcctgagt agcaggtggc ggcagcgctc 360
aagcctgcgc ccgcgcccgc ctctacccc cctgcccgcg acggcgcccc cagcgcgcca 420
cccccgagc gcctgctcgc ctctcccgac ctggggctgc tgaagctggc ctcccccgag 480
ctcgagcgcc tcatcatcca gtccaacggg ctggtcacca ccacgccgac gagctcacag 540
ttcctctacc ccaaggtggc ggccagcgag gaggcaggat tcgccagggg cttcgtcaag 600
gccctggagg atttacacaa gcagaaccag ctggcgcgcg gccgggc cgc tgccgcggcc 660
gccgccgccc ccgggggggc ctcgggcacg gccacgggct ccgcgcccc ccggcagctg 720
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153/292

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gccccggcgg cggccgcgcc cgaagcgcct gtctacgcga acctgagcag ctacgcgggc 780
ggcgccgggg gcgcgggggg cgccgcgacg gtcgccttcg ctgccgaacc tgtgcccttc 840
ccgcccggcg cacccccagg cgcgt tgggg ccgcccgcgcc tggctgcgct caaggacgag 900
ccacagacgg tgcccagcgt gccgagcttc ggcgagagcc cgccgttgct gcccatcgac 960
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caggctccgg cgtactgagt cgggcatggc ggccacctcc aaggggcggg ctgcgggggg 1260
ggtgtcgtgg gcgcccggga cttggagagg gtgcggccct ccaccccccc ctcccagagt 1320
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gcgtctcggc tgccc ctttg tacaccgcgc cgcaagggg ctccgagggg gcgcacgtca 1560
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gttcgattct gccctattta tgttctact cggggaacaa acgttggttg tgtgtgtgtg 1680
tgttttcttg tgttggttt ttaagaaat aaaaaaatt ctcc gccct 1740
ttctcgatc tcgctcccc ttcggtctt cgaccgtccc cccctcccct tttttgttc 1800
tgttttgtt tgttttcta cgagtcaca ttctgtttg taatccttg ttcgcccgt 1860
tttctgttt cagtaaagtc tcgttacgcc a 1891
```

<210> 235

<211> 421

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(421)

<223> 3' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of
chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 235

```
accaaaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg gagcatgagg 60
aggaaaatga ggaagaagat gaagtaccgg acgatgagac tctgaaccaa atgattgctc 120
gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg agggaagatg 180
cccggaaacc gaaacggaag ccccgtttaa tggaggagga tgagctgcc tctggntca 240
ttaaggatga cgtggaagta gaaaggctca cctgtgaaga agaggaggag aaaatatttg 300
ggagggggtc ccgcagcgc cgtgacgtgg actacagtga cgccctcac gagaagcagt 360
ggctaaaggg cntcgaaga cggcatttng gaggaattng aagaggaata c ggtaagaa 420
g 421
```

<210> 236

<211> 438

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(438)

<223> 5' terminal sequence. swi/snf related,
matrix associated, actin dependent regulator of

chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 236

```

tgccaatttt ctgccgggca ctcttaaaca ctgactgtaa gacgatggag tcttcataga 60
tctgggatcc ctccagggtg aacgtctgag cg ttgtgaca gagaagcatg acatccttct 120
ccaggctgcc taggctccgg tacttatgat tacgaatcct ttcctttatt tttttgaaat 180
ccactggctt cctaattaat tcatagtatt ctggtaattc tttccttgaa ggtaactgaa 240
tgaagacttc actgagctgt cgccctgaac tgtttccttc tatttccaac tgagaattac 300
tgggcacctt ctccacgtta caccatctct tgtagtttat cacagtattc gatgattagc 360
gttcatctgg ctttgtcagt ttggggggga tttggtgaca gntttntcag cgggaggggc 420
gcctcttctc ttcttagg                                438

```

<210> 237

<211> 5257

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5257)

<223> swi/snf related, matrix associated, actin
dependent regulator of chromatin, subfamily a,
member 2 (SMARCA2) gene.

<400> 237

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aaaaattttc tgttacaaa ttttacaact tctaataaga ctactataac tttatgtaaa 60
ctgatgaaga tggctgatt aacatattct gtgatatggt ttacaacttt taatcataat 120
tgtccatgat tttggaatgc tgttatttat cagtaaatgt aaaatatgtg aggcatttag 180
ccatacacac actagaactt tttaaaactt tgcctatag tgtaatta ta aactgatgac 240
tattatcttc atacattgag tcttcatgca tcaatgaaat gaaaaatata ggagtagatg 300
tccacgcccc cagaccctgg tgcgatgccc caccagggc cttcgccggg gcctgggcct 360
tcccctgggc caattcttgg gcctagtcca ggaccaggac catccccagg ttccgtccac 420
agcatgatgg ggccaagtcc tggacc tcca agtgtctccc atcctatgcc gacgatgggg 480
tccacagact tccacagga aggcattgat caaatgcata agcccatcga tggatatacat 540
gacaagggga ttgtagaaga catccattgt ggatccatga agggcactgg tatgcgacca 600
cctcacccag gcatggccc tcccagagt ccaatggatc aacacagcca aggttatatg 660
tcacacacac catctccatt aggagcccca gagcagctct ccagccctat gtctggagga 720
ggcccaactc cacctcagat gccaccaagc cagccggggg ccctcatccc aggtgatccg 780
caggccatga gccagcccaa cagaggtccc tcacctttca gtctgtcca gctgcatcag 840
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caacagcagc agcagcagca gcagcagcag cagcagcagc agcaacagca gccgcagcag 1020
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ccatctggcc cggggccgga gc tgagcggc ccgagcacc cgcagaagct gccggtgcc 1140
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agaatgcggc gactgatggc tgaagatgag gagagttata gaaaactgat tgatcaaaag 1860
aaagacaggc gtttagctta ccttttgtag cagaccgatg agtatgtagc caatctgacc 1920

```

aatctggttt gggagcacia gcaagcccag gcagccaaag agaagaagaa gaggaggagg 1980
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gcactgggtt gtttctatat catcatcgtc tataaactag ctttaggata gtgccagaca 5160
aacatatgat atcatggtg aaaaaacaca cacatacaca aatatttgtg accaa atggg 5220
cctcaaagat tcagattgaa acaaaacaaa agctttt 5257

<210> 238

<211> 507

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(507)

<223> 3' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma
isoform (PPP2R2C) gene.

<400> 238

```
tacatgctca cccgggacta cttacagtc tatggatggg acctgaacat ggaggcaaga 60
cccatagaga cctaccaggt ccatgactac cttcggagca agctctgttc cctgtacgag 120
aacgactgca ttttcgacaa gtttgaatgt gcctggaacg ggagcgacan tncatcatga 180
ccggggccta caacaacttc ttccgcatgt tcgatcgga caccaagcgg gacgtgacct 240
tgggaggcct cgagggaag cagcaagccc cgggctgtgc tcaagccacg gcgctgtgc 300
gtgggggggc aagcgccggc gtgnatga ca tcagtgtggg acagcttggg acttcaccaa 360
gaagatcctg cacacggcct ggcacccggc tgaggaacat catttgccat tcgccgccac 420
caacaacctg ttacatcttt ccaggggcaa ggtaaatttt tgacattgca ttaggtattn 480
tgcaatttcc cggnccttgc caacca 507
```

<210> 239

<211> 521

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(521)

<223> 5' terminal sequence. protein phosphatase 2
(formerly 2a), regulatory subunit b (pr 52), gamma a
isoform (PPP2R2C) gene.

<400> 239

```
taaacagaca attactgcc aacacaattc tggcctagga aagcggggnn gggagggggc 60
ccaaacttcc tgtgtccaca cactgccacc tctgcagctg tcctcatcag tgggtgtgact 120
ttcttccct cttgcattg cggtcgtgaa ggtcatgtcg gggatgactt gcatgaggct 180
gggtggcagg ggccgggaac tgcacatacc tagtgcattg cagagtttac cttgtcctgg 240
aagatgtaca ggttgttggg ggcggcgatg gcaatgatgt tctcagccgg gtgccaggcc 300
gtgtgcagga tcttcttggg gaagtccaag ctgttccaaa atgatgtcat cagccgggcc 360
cttgcccccc acgnaaangg nccnttggtt tnagcaaagc ccng ggtttg ttgcttttcc 420
ctngnaggcn tncaggntca agtnccnttt ggtnttncce gatcgaacat ncggaagaat 480
tttttttagg ccccentcat gatgaacgtg tncgttccct t 521
```

<210> 240

<211> 350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(350)

<223> 3' terminal sequence. thrombospondin 3
(THBS3) gene.

<400> 240

```
cagattcatt nnnngganntg cctgtgacaa ttgccccaac gttcccaaca atgaccagaa 60
ggacacagat ggcaatgggg aaggagatgc ctgtgacaac gac gtggatg gggatgggtgc 120
aggcctgggg ctgaaggggt ggctggggga cctgtgagaa tttggatcag gtggggatga 180
agcagggaag ctaggaagtc tctgtgaaat agggaggcag gcttntggac gttggcctgg 240
gtgaggagag attacctgca gcagatgtca ataggaatnt gaggtagggc gtagtnttag 300
gcagagtttg gactagaggg t nagacaaga aacaggcaga tttcctggcc 350
```

<210> 241

<211> 2871

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2871)

<223> thrombospondin 3 (THBS3) gene.

<400> 241

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atggagacgc aggaacttcg gggggccctg gctcttctcc tcctttgctt tttcacatct 60
gccagtcagg atctgcaggt aattgacctg ctgactgtgg gcgagtctcg gcagatggta 120
gctgtggcag agaagatccg gacagccttg ctcactgctg gggacatcta cctcttatcc 180
accttccgcc tgccccccaa gcagggtggg gtcctctttg g cctctatcc tcgccaagac 240
aacactcgat ggctggaggc ctctgtttga ggcaagatca acaaagtact ggtgcgatac 300
cagcggggagg atggcaaaagt ccacgccgtg aacctacagc aagcgggcct ggctgatggg 360
cgcacacaca cagttctcct gcgactccga ggtccctcca gaccagccc tgccctacat 420
ctctacgtgg actgcaaaact gggtgacca catgcaggcc ttccagcact ggccccatt 480
cctccagcgg aggtcgatgg gctggagatt aggactggac agaaggcgta tttgaggatg 540
cagggcctttg tggaaatctat gaaaattatt ctgggtgggt ccatggcccg ggtaggagcc 600
ctgagtgaat gtccattcca aggggacgag tccatccaca gtgcagtga caatgcactg 6 60
cactccattc taggggagca gaccaaggcg ctggtcacc aactcaccct cttcaaccag 720
atcctgggtg agctgcggga tgatatacga gaccaggtaa aggaaatgtc cctgatccga 780
aacaccatta tggagtgtca ggtgtgcggc ttccatgagc agcgttccca ctgcagcccc 840
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ctgtgtccca acaagacca gcagaactca gatacagatt catttggtga tgccctgtgac 1620
aattgcccc aagttcccaa caatgaccag aaggacacag atggcaatgg ggaaggagat 1680
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tgtgatacta atgaagacag cgatggggat gggcatcagg acaccaagga caactgcccc 1920
cagctgccaa atagctccca gctggactct gataacgatg gac ttggaga tgagtgtgat 1980
gggatgatg acaatgatgg catccagat tatgtgcctc ctggtcccg taactgccgc 2040
```


158/292

```

ctggtaccca atcccaatca gaaggactca gatggcaatg gcgttggtga tgtgtgtgag 2100
gatgactttg acaatgatgc tgtggtcgac cccctggatg tgtgtcctga aagtgcagag 2160
gtaacgctta cggatttt cg ggcctatcag accgtcgtcc tggatcctga gggatgatgct 2220
cagattgacc caaactgggt tgtgctcaac cagggcatgg aaatcgttca gaccatgaac 2280
agtgaccctg gcttggcagt tggatacacg gccttcaatg gtgtggactt tgaaggcacc 2340
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gtggcgggatt ctggggtgat cattgacaca tccatgcgag gggggcgtct tgggtgtattc 2760
tgcttctccc aagaaaacat aatttgggcc aatctccagt atcgatgcaa tgacacagt 2820
cctgaggact ttgagccatt ccggaggcag ctgctccagg gaagggtgtg a 2871

```

<210> 242

<211> 509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(509)

<223> 3' terminal sequence. actin, gamma 1 (ACTG1)
gene.

<400> 242

```

cacttttatt ttnccttaca caatgacgtg ttgctggggc ctaatgttct cacataacag 60
tagaaaacca aaatttggtg tcatctcttc aaagantcga ganttgcgta caaaaaaac 120
cttacataan ttaagantga ntacatttac aggcgtaaat gcaaaccgnt tccaactcaa 180
agcaagtaac agcccacggt gttctggcca aagacatcag ctaagaaagg aaactggggn 240
ctacggctt gggactttcc aacctggac aggaccgca agncaaac aactgggttc 300
ttgccagcct ctaggaggaa ttcccgaac actcaggccc tggacangtt taataccagg 360
ggggancagt taactttcan tacaggggnc aaaatcaggc aacagttt tt accantccag 420
tggttggttt cnggttacag gtttcagggg cattttnttt tcggaggggt tntccogtt 480
tcgtgagggt aggtgagggt tttntgctt 509

```

<210> 243

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(393)

<223> 5' terminal sequence. actin, gamma 1 (ACTG1)
gene.

<400> 243

```

gatcacgcc ctggccccag caccatgaag atcaagatca tcgcaccccc agagcgcaag 60
tactcgggtg ggatcgggtg ctccatcctg gcctcactgt ccaccttc a gcagatgtgg 120
attagcaagc aggagtacga cgagtcgggc ccctccatcg tccaccgcaa atgcttctaa 180
acggactcag cagatgcgta gattttgctg catgggttaa ttgagaatag aaatttgccc 240

```

159/292

ctgggaaatt gcacacacct catgctagcc tcacgaaact gggaataagc ctttcgaaaa 300
gaaattgtcc ttgaagcttg tatctgg tat cagcactggg ntgttaggaa ntgttgctg 360
atttttgacc ttgtanttga agtttaactg ttt 393

<210> 244

<211> 1919

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1919)

<223> actin, gamma 1 (ACTG1) gene.

<400> 244

gtctcagtcg ccgctgccag ctctgcact ctgtttcttc gccgctccgc cgtcgcgttt 60
ctctgccggt cgcaatggaa gaagagatcg ccgcgctggt cattgacaat ggctccggca 120
tgtgcaaaagc tggttttgct ggggaacgac ctccccgagc cgtgtttcc t tccatcgtcg 180
ggcgccccag acaccagggc gtcatggttg gcatgggcca gaaggactcc tacgtggcg 240
acgaggccca gagcaagcgt ggcatcctga cctgaagta cccattgag catggcatcg 300
tcaccaactg ggacgacatg gagaagatct ggcaccacac ctctacaac gagctgcgcg 360
tggccccgga ggagcaccca gtgctgc tga ccgaggcccc cctgaacccc aaggccaaca 420
gagagaagat gactcagatt atgtttgaga ccttcaacac cccggccatg tacgtggcca 480
tccaggccgt gctgtccctc tacgcctctg ggcgcaccac tggcattgtc atggactctg 540
gagacggggt caccacacag gtgcccattc acgagggcta cgcctcccc cagcccatcc 600
tgctcttgga cctggctggc cgggacctga ccgactacct catgaagatc ctactgagc 660
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tgtgtacagt cgccctggac ttcgagcagg agatggccac cgccgcatcc tcctcttctc 780
tggagaagag ctacgagctg cccgatggcc aggtcatcac cattggc aat gagcggttcc 840
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cgcaattctc gattctttga agagatgaca acaaattttg gttttctact gttatgtgag 1860
aacattagga cccagcaaca cgtcattgtg taaggaaaaa taaaagtgtc g ccgtaacc 1919

<210> 245

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(467)
<223> 3' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 245
ccgccgcgcg gcagctgtgc ttgctctacc tgtcggcggg gctcctgtcc cggctcggcg 60
cacttncaac ttggacactc gggaggacaa cgtgatcccg aaatatggag accccgggag 120
cctcttcggc ttctcgctgg ccatgcactg gcaactgcag cccgaggaca agcggctgtt 180
gctcgtgggg gcccgcggg agnaagcgt tccactgcag agagccaac a gaacgggagg 240
gctgtacagc ttgcgacatc accgcccggg ggccatgcac ggggatcgag ttnataacg 300
atgcttgacc ccacgtcaga aagcaaggaa gattagtgg atngggggtc aacgtccaga 360
gccaaaggttc agggggcaag gtogtgacat gtgttnaccc tattgaaaaa aggcagcgtt 420
ttattacgna gcangatttc cgagaca ttt ttgggcgttt tttttcc 467

<210> 246
<211> 473
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(473)
<223> 5' terminal sequence. integrin, alpha 6
(ITGA6) gene.

<400> 246
gccctctccc atccatatcg ttttcaatcc tgagattctg actcaggaca naacaccgcc 60
caaagatgtc tcgggattcc tgcttcgtat taacatgctg ccttttttca tatcggtgag 120
cacatgtcac gaccttgccc cctggacctt ggctctggac ggtgaccccc atccactgat 180
cttccttgct ttctgacgtg gggtc agcat cgttatcaaa ctcgatccgc gtgcatggcc 240
cccggcggtt ggatgtcgca gctgtacagc cctcccgttc tgttggtct ctgcagtggg 300
aagcgcttct gcccgcgggg cccccacgga gcaacagccg cttgtcctcg ggetgcagtt 360
gccagtgcac gggccagcga gaaagccgaa gaggttcccc ggggtnttcc atattttccg 420
gatcaagttg ttcctnccga gttttccaag tttgaagggt tgcgcaaggc cgt 473

<210> 247
<211> 5611
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5611)
<223> integrin, alpha 6 (ITGA6) gene.

<400> 247
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<210> 248

<211> 406

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(406)

<223> 3' terminal sequence. rad9 (s. pombe)
homolog (RAD9) gene.

<400> 248

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cgntgctatt gattcattaa aaaaagaaaa gaaaaa taca ccaaggttcc atnttccccg 240
tgacaggtgg gccnagggg tgggggtnac cccccccag natggcagca tgattntnt 300
acaatcaatc catcatntgg ggcacagggt ggttttcggg ggctattntt tggctttggc 360
gaaattncgg gntggggttaa tgggtnggcc tccagggtta aggcca 406

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<210> 249

<211> 2102

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2102)

<223> rad9 (s. pombe) homolog (RAD9) gene.

<400> 249

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ggccgtccac tccctgtccc gcatcgggga cgagctctac ctggaaccct tggaggacgg 180
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cgttgccctg agctgcagcc tcggccccag gatcctgctc acagtcaccg caggtgcagg 2040
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at 2102
```

<210> 250

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 250

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tacagaaaat tgtaatgata ccattgagta caattaaaca ctctgagaat ttcacagaaa 120
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agctgcaaac accctgggcc agatttctta aaacagctac atgacaaaaa caatgctatt 240
gacatccaat aatgctaaag cctgggtacc acccggtcc cactgactgt ggn ttccaaa 300
catctctcca ctgactgtgg ntttcaaccn caaggnaagg gaaatgggat attccttggg 360
ctctt 365

<210> 251

<211> 453

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(453)

<223> 5' terminal sequence. activating
transcription factor 3 (ATF3) gene.

<400> 251

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gcaacggcca gggttgtgct ttctagcaaa tatgctgt ta tgtccagaaa ttgtgtgtgc 120
aagaaaacta ggcaatgtac tcttcgatg tttgtgtcac acaacactga tgtgactttt 180
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tgcatgatct caagatattc aggtgggcca gaagagcttg tcagcaagag ggagggacag 300
aattctccca ggcgtt aaca caaaatccat ggggcagtat ggatgggcag gtccntctgt 360
tggcaaactc agttcccaag tcacagggaa gganaggcag gaaagtttca actttcccaa 420
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<210> 252

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> activating transcription factor 3 (ATF3)
gene.

<400> 252

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gagaagctgg aaagtgtgaa tgctgaactg aaggctcaga ttgaggagct caagaacgag 720
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165/292

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aattctgatg tttctgtgaa attctcagag tgtttaattg tactcaatgg tatcattaca 1980
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<210> 253

<211> 502

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(502)

<223> 3' terminal sequence. v-akt murine thymoma
viral oncogene homolog 2 (AKT2) gene.

<400> 253

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acggggttgc nggggtgttt ctgggaggga cccggttttt cggttgattn ttttgaggcg 480
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<210> 254

<211> 1715

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1715)

<223> v-akt murine thymoma viral oncogene homolog
2 (AKT2) gene.

<400> 254

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ggttttatgg tgacagatt gtctcggtc ttgagtactt gactcgcgg gacgtggtat 1020
accgcgacat caagctggaa aacctcatgc tggacaaaga tggccacatc aagatcaactg 1080
actttggcct ctgcaaagag ggcacagtg acggggccac catgaaaacc ttctgtggga 1140
ccccggagta cctggcgccg gaggtgctgg aggacaatga ctatggccgg gccgtggact 1200
ggtgggggct ggtgtgtggtc atgtacgaga tgatgtgcgg ccgcctgccc ttctacaacc 1260
aggaccacga gcgcctcttc gagctcatcc tcatggaaga gatccgcttc ccgcgcacgc 1320
tcagccccga ggccaagtcc ctgcttgctg ggctgcttaa gaaggacccc aagcagaggc 1380
ttggtggggg gccagcgat gccaaggagg tcatggagca caggttcttc ctcagcatca 1440
actggcagga cgtggtccag aagaagctcc tggcaccctt caaacctcag gtcaggtccg 1500
aggtcgacac aaggtacttc gatgatgaat ttaccgccca gtccatcaca atcacacccc 1560
ctgaccgcta tgacagcctg ggctt actgg agctggacca gcggaccac ttccccagt 1620
tctctactc ggccagcatc cgcgagttag cagtctgcc acgcagagga cgcacgctcg 1680
ctgccatcac cgctgggtgg ttttttacc ctgcc 1715
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<210> 255

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 5' terminal sequence. s100 calcium-binding
protein, beta (neural) (S100B) gene.

<400> 255

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gagaggatgt ctgagctgga gaaggccatg gtggcctcat cgacgttttc caccaatatt 60
ctggaaggga gggagacaag cacaagctga agaaatccga actcaaggag ctcacaaaca 120
atgagctttc ccatttctta gaggaatca aagagcagga ggttgtggac aaagtcatgg 180
aaacactgga caatgatgga gacggcgaat gtgacttcca gggaattcat ggcctttgtt 240
gccactggtta ctactgcctg ccacgagttc ttgaacat g agtnagatta ggaaagcagc 300
caaacctttt cctgttaaca gaggacggtt catggcaaga naggcaggac aggcaagggg 360
tttgaggct tagttaggga gcttgagggt tttccagccg tntttnttg gttaatttag 420
ggaaggtttg a 431
```

<210> 256

167/292

<211> 1095
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1095)
<223> s100 calcium-binding protein, beta (neural)
(S100B) gene.

<400> 256
tgccgcccag gacccgcagc agagacg acg cctgcagcaa ggagaccagg aaggggtgag 60
acaaggaaga ggaagtctga gctggagaag gccatggtgg ccctcatcga cgttttccac 120
caatattctg gaaggaggag agacaagcac aagctgaaga aatccgaact caaggagctc 180
atcaacaatg agctttccca tttcttagag gaaatcaaag agcaggaggt tgtggacaaa 240
gtcatggaaa cactggacaa tgatggagac ggcgaatgtg acttcagga attcatggcc 300
tttggtgccca tggttactac tgcctgccac gagttctttg aacatgagtg agattagaaa 360
gcagccaaac ctttcctgta acagagacgg tcatgcaaga aagcagacag caagggcttg 420
cagcctagta ggagctgagc tttccagccg tgtttagct aattagga ag cttgatttgc 480
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acttaggagt caggtctcag tgataaagcg tgcaccgtgc agcccgccat ggccgtgtag 660
accctaaccg ggagggaacc ctgact acag aaattacccc ggggcaccct taaaacttcc 720
actaccttta aaaaacaaag ccttatccag cattatttga aaacactgct gttctttaa 780
tgcgttcttc atccatgcag ataacagctg gttggccggg gtggccctgc aagggcggtg 840
tggtcttcgc ctgcttcccg ggatgcgcct gatcaccagg tgaacgctca gcgctggcag 900
cgctctggaa aaagcaactc catcagaact cgcaatccga gccagctctg ggggctccag 960
cgtggcctcc gtgacctatg cgattcaagt cgcggtgca ggatccttgc ctccaacgtg 1020
cctccagcac atgcggcttc cgagggcact accgggggct ctgagccacc gcgagggcct 1080
gcgttcaata aaaag 1095

<210> 257
<211> 542
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(542)
<223> 3' terminal sequence. atp -binding cassette,
sub-family b (mdr/tap), member 1 (ABCB1) gene.

<400> 257
ttttaaaatc tactttaatt ctgttataaa atttataatg cagttttaaac tatgatttct 60
ctccacttga tgatgtctct cactctgttc ctttaattac gaagtctctg aagactctga 120
acttgactga ggaaatgtta aacagatacc tcttcataat tctgtaagtg tttgctttta 180
actttgaata aatgtcatat ctaaacaaat attaaaaagt atttaacatc tcatacagtc 240
agagttcact ggcgctttgt tccagcctgg aactgacca ttgaaaaata gatgccttcc 300
tgtgccagca gctgctgatg cgtgccatgc tccttgactc tgccattctg aaacaccact 360
attaagtctg cattctggat ggtggacagg cggtagcaaa tcacaatgca ggtgcggcct 420
tctctggcta tgccagggct tcttgacaaa ctttttacc tactgtatcc agagctgacg 480
tggtctatcc aaaagcaaaa tantgggctg tctaacaagg gcacgagcta ttgcatgcg 540
tt 542

<210> 258
<211> 4643
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4643)
<223> atp-binding cassette, sub-family b
(mdr/tap), member 1 (ABCB1) gene.

<400> 258
cctactctat tcagatattc tccagatt cc taaagattag agatcatttc tcattctcct 60
aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120
tcctcctgga aattcaacct gtctcgaggt ttctcgagga atcagcattc agtcaatccg 180
ggccgggagc agtcatctgt ggtgaggctg attggctggg caggaacagc gccggggcgt 240
gggctgagca cagcgcttcg ctctctttgc cacaggaagc ctgagctcat tcgagtagcg 300
gctcttccaa gctcaaagaa gcagaggccg ctgttcgttt cctttaggtc tttccactaa 360
agtcggagta tcttcttcca agatttcacg tcttggtggc cgttccaagg agcgcgagg 420
cgggatggat cttgaagggg accgcaatgg aggagcaaag aagaagaac t tttttaaaact 480
gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540
gtttcgctat tcaaattggc ttgacaagtt gtatatggtg gtgggaactt tggctgccat 600
catccatggg gctggacttc ctctcatgat gctgggtgtt ggagaaatga cagatatctt 660
tgcaaatgca ggaattttag aagatct gat gtcaaacatc actaatagaa gtgatatcaa 720
tgatacaggg ttcttcatga atctggagga agacatgacc aggtatgcct attattacag 780
tggaattggt gctggggtgc tgggtgctgc ttacattcag gtttcatttt ggtgcctggc 840
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atttttcact gggtttatag taggatttac acgtgggttg aagctaacc ttgtgatttt 1080
ggccatcagt cctgttcttg gactgtcagc tgctgtctgg gcaaa gatac tatcttcatt 1140
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agcagcttat gaaatcttca agataattga taataagcca agtattgaca gctattcga a 1560
gagtgggcac aaaccagata atattaagg aaatttgaa ttcagaaatg ttcacttcag 1620
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gcagacggtg gccctgggtg gaaacagtg ctgtgggaag agcacaacag tccagctgat 1740
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cataaatgta aggtttctat gggaaatcat tgggtgtgtg agtcaggaac ctgtattgtt 1860
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tgagaaagct gtcaagggaag ccaatgccta tgactttatc atgaaactgc ctcataaatt 1980
tgacaccctg gttggagaga gaggggcca gttgagtgtt gggcagaagc agaggatcgc 2040
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gaccaccatt gtgatagctc atcgtttgtc tacagttcgt aatgctg acg tcatcgttg 2220
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cattacttcc aaacttgtca caatgcagac cagaggaat gaagttgaat tagaaaaatgc 2340
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aatggaggc ctgcaaccag catttgcaat aatattttca aagattatag gggtttttac 2640
aagaattgat gatcctgaaa caaacgcaca gaatagtaac ttgttttcac tattgtttct 2700

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aatagaaaac ttccgaaccg ttgtttcttt gactcaggag cagaagtgtg aacatatgta 3180
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tacattttcc ttaccacagg caatgatgta tttttcctat gctggatgt t tccggtttgg 3300
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ctacagcagc gaaggcctaa tgc cgaacac attggaagga aatgtcacat ttggtgaagt 3540
tgtattcaac tatcccaccc gaccggacat ccagtgctt cagggactga gcctggaggt 3600
gaagaagggc cagacgctgg ctctgggtgg cagcagtggt tgtgggaaga gcacagtgtt 3660
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aataaagcga ctgaatgttc agtggctccg agcacacctg ggcatcgtgt ccaggagcc 3780
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attcaaaagt aaaagcaaac acttacagaa ttatgaagag gtatctgttt aacatttctt 4380
cagtcaagtt cagagtcttc agagacttcg taattaaagg aacagagtga gagacatcat 4440
caagtggaga gaaatcatag tttaaactgc attataaatt ttataacaga attaaagtag 4500
attttaaaag ataaaatgtg taattttgtt tataatttcc catttggtgact gtaactgact 4560
gccttgctaa aagattatag aagta gcaaa agtattgaa atgtttgcat aaagtgtcta 4620
taataaaact aaactttcat gtc 4643
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<210> 259

<211> 486

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(486)

<223> 3' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 259

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aaaattataa aatattttta gttataattt aaaattctca ataaaaactca aacacaaacc 1 20
acactgggat ttcacacagc taattttctaa tgcagtttac ataaatattt acaacactta 180
aacaatttca aagaaaaata cactgtattc catacatagc ctgatcacag tagttgttct 240
ctcttatttc ccagagtttt tctgcccctt taaaaggaa cctctggctgt tctgancctt 300
atcacatctc tgttttgact gttgggcttt ggttgggtgc cagtgggttc gccaggaaact 360
tctctgggaa actttttttt tcaacactgg ctagggtang gggngttag gggggnggt 420
ttggtttcnt cacantccct cagggtnggg ggcgggtng ggnattacc ggcgggggt 480
tttttc 486
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<210> 260
<211> 478
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(478)
<223> 5' terminal sequence. selectin e
(endothelial adhesion molecule 1) (SELE) gene.

<400> 260
gcctactatg ccagatgcct ttatggctga aaccgcaaca cccatcacca cttcaataga 60
tcaaagtcca gcaggcaagg acggccttca actgaaaaga ctcagtgttc cctttcctac 120
tctcaggatc aagaaagtgt tggctaata agggaaagga tttttcttc caagcaaagg 180
tgaagagacc aagactctga aatctcagaa ttcttttct aactctccct tgctcg ctgt 240
aaaatcttgg cacagaaaca caatattttg tggctttctt tcttttgccc ttcacagtgt 300
ttcgacagct gattacacag ttctgtcat aaggaatgaa taattaatta tccagagttt 360
agaggaaaaa aatgactaaa aatattatta acttaaaaaa tggacaggtg ttggatgccc 420
acaggcaaat gcatgggggg gttgtttaat gggt gcaaat ccctacttga atgctctt 478

<210> 261
<211> 3834
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3834)
<223> selectin e (endothelial adhesion molecule 1)
(SELE) gene.

<400> 261
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ccaaaacgga aagtatttca agcctaaacc tttgggtgaa aagaactctt gaagtcata 120
ttgcttcaca gttctctca gctctcactt tgggtgcttct cattaaagag agtggagcct 180
ggtcttacaa cacctccacg gaa gctatga cttatgatga ggccagtgtt tattgtcagc 240
aaaggtacac acactgggtt gcaattcaaa acaaagaaga gattgagtac ctaaaactcca 300
tattgagcta ttcaccaagt tattactgga ttggaatcag aaaagtcaac aatgtgtggg 360
tctgggtagg aaccagaaa cctctgacag aagaagccaa gaactgggct ccaggtgaac 420
ccaacaatag gcaaaaagat gaggactgag tggagatcta catcaagaga gaaaaagatg 480
tgggcatgtg gaatgatgag aggtgcagca agaagaagct tgccctatgc tacacagctg 540
cctgtaccaaa tacatcctgc agtggccacg gtgaatgtgt agagaccatc aataattaca 600
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acaattcttc ctgctctatc agctgtgata ggggttacct gccaaagcagc atggagacca 780
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 ggtaaaaagt acttattcta gattaccccc tcattgttta ttaacaaatt atgttacatc 2760
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 tttaaattat aacttaaaat attttataat ttttaaagta tatatttatt taagcttatg 3780
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<210> 262

<211> 267

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(267)

 <223> 3' terminal sequence. epidermal growth
 factor (beta-urogastrone) (EGF) gene.

<400> 262

gtttatgttt ttggtgattt tatttaaata attagaagaa attcatcgtt gt ctataatg 60

172/292

```

aaaacaaatc aggcaattta cttacaatct tgtaactgaa aatacatata aattctgtgc 120
aatcacacca agagggaataa ttctgtaggg gaaaaggaca gtaatgacta agaaactccg 180
aagcctcctg tgtaatatct taaaatanaa tgttttcatt caaatatctt aaaaaataag 240
natctaactc gaaaaaatca gtttcta                                267

```

<210> 263

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 5' terminal sequence. protein kinase c
substrate 80 k-h (PRKCSH) gene.

<400> 263

```

ggagtcaggag gtgcaggggg agcagcccaa gccggccagc cctgctgagn gaagacaaaa 60
tncgcacctc cgacgagcag acgcaggcct tcatcgatgc tgcccaggag gcccgcaaca 120
agttcgaggga ggccgagcgg tcgctgaagg acatggagga gtccatcagg aacctggnag 180
caaganatct cttttgactt tggccccaac ggnagtcttg cttacctgta cagccagtgc 240
tacgagctca ccaccaacga atacgtctac cgcctctncc ccttcaagct tgtnttcgna 300
gaaacccaaa ctcggggggt ctcccaccag ccttggcacc tgggggcttc atgggattgg 360
gcccgacca cnacaatttc agt                                383

```

<210> 264

<211> 2056

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2056)

<223> protein kinase c substrate 80k -h (PRKCSH)
gene.

<400> 264

```

ggaaccgcgg ctgctggaca agaggggtgc ggtggatact gacctttgct ccggcctcgt 60
cgtgaagaca cagcgcatct ccccgtgta ggcttctccc acagaaccgg ttctgggcct 120
cagagcgtct ggtgagatgc tgttgccgct gctgctgctg ctacctatgt gctgggccgt 180
ggaggtcaag aggccccggg gcgtctccct caccaatcat cacttctacg atgag tccaa 240
gcctttcacc tgcctggagc gttcggccac catcccattt gatcaggta acgatgacta 300
ttgcgactgc aaagatggct ctgacgagcc aggcacggct gcctgtccta atggcagctt 360
ccactgcacc aacactggct ataagcccct gtatatcccc tccaaccggg tcaacgatgg 420
tgttttgtgac tgctgcgatg gaacagacga gta caacagc ggcgtcatct gtgagaacac 480
ctgcaaaagag aagggccgta aggagagaga gtccctgcag cagatggccg aggtcaccgg 540
cgaagggttc cgtctgaaga agatccttat tgaggactgg aagaaggcac gggaggagaa 600
gcagaaaaag ctcttgagc tacaggctgg gaagaagtct ctggaagacc aggtggagat 660
gtcgcggaca gtgaaggagg aagctgagaa gccagagaga gaggccaaag agcagacca 720
gaagctgtgg gaagagcagc tggctgctgc caaggcccaa caggagcagg agctggcggc 780
tgatgccttc aaggagctgg atgatgacat ggacgggacg gtctcgggtga ctgagctgca 840
gactcaccgg gagctggaca cagatgggga tggggcggtt tcagaagcgg aag ctcaggc 900
cctcctcagt ggggacacac agacagacgc cacctctttc tacgaccgcg tctgggccgc 960

```

173/292

```

catcagggac aagtaccggt ccgaggcact gccaccgac cttccagcac cttctgcccc 1020
tgacttgacg gagcccaagg aggagcagcc gccagtgcc tcgtcgccca cagaggagga 1080
ggaggaggag gaggaggagg aagaagaggc tgaagaagag gaggaggagg aggattccga 1140
ggagggccca ccgccactgt ccccccgca gccggccagc cctgctgagg aagacaaaat 1200
gccgccctac gacgagcaga cgcaggcctt catcgatgct gcccaggagg ccgcaacaa 1260
gttcgaggag gccgagcggg cgctgaagga catggaggag tccatcagga acctggagca 1320
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gggcccaggc ggggtgggtc cacattccca ggcccaca gcctccaaag atgggtaaa 1920
gagcttgccc tccctgggccc cccacacctg gtgactcgcc ccaccacccc cagccct gtc 1980
cctgccaccc ctctagtgg ggactagtga atgacttgac ctgtgacctc aatacaataa 2040
atgtgatccc ccaccc                                     2056

```

<210> 265

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc_feature

<222> (1)..(379)

<223> 5' terminal sequence. diphtheria toxin
receptor (heparin-binding epidermal growth
factor-like growth factor) (DTR) gene.

<400> 265

```

ggttctgtga cccatctgta gtaatttatt gtctgtctac atttctgc ag atcttccgtg 60
gtcagagtgc cactgcggga ntctgtatgg tcaggatgta ggggttaact tggtcagagc 120
cactctatga gttggacttc agtcttgccct aggcgatttt gtctaccatt tgtgttttga 180
aagcccaagg tgctgatgtc aaagtgtaac agatatcagt gtctccccgt gtcctctccc 240
tgccaagtct cagaagaggg tgggctt cca tgcctgtagc tttcctgggc cctcaccccc 300
atggccccag gccacagcg tggagactnc actttnccct tgtgtcaaga catttctctn 360
aactcctgnc attcttctg                                     379

```

<210> 266

<211> 2360

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2360)

<223> diphtheria toxin receptor (heparin-binding
epidermal growth factor-like growth factor) (DTR)
gene.

<400> 266

```

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gggcgggctg agtgagcaag acaagacact caagaagagc gagctgcgcc tgggtcccgg 120
ccaggcttgc acgcagaggc gggcggcaga cgggtgcccg cggaatctcc tgagctccgc 180
cgcccagctc tggtgccagc gcccagtggc cgccgcttcg aaagtgactg gtgcctcgcc 240
gcctcctctc ggtgcgggac catgaagctg ctgccgtcgg tggtgctgaa gctctttctg 300
gctgcagttc tctcggcact ggtgactggc gagagcctgg agcggcttcg gagagggcta 360
gctgctggaa ccagcaaccc ggaccctccc actgtatcca cggaccagct gctaccacct 420
ggaggcgggc gggaccggaa agtccgtgac ttgcaagagg cagatctgga cctttt gaga 480
gtcactttat cctccaagcc acaagcactg gccacaccaa acaaggagga gcacgggaaa 540
agaaagaaga aaggcaaggg gctagggaag aagagggacc catgtcttcg gaaatacaag 600
gactttctga tccatggaga atgcaaatat gtgaaggagc tccgggctcc ctctctgcatc 660
tgccaccggg gttaccatgg agagaggtgt catg ggctga gcctcccagt ggaataatgc 720
ttatatacct atgaccacac aaccatcctg gccgtgggtg ctgtgggtct gtcactgtgc 780
tgtctgctgg tcatcgtggg gcttctcatg tttaggtacc ataggagagg aggttatgat 840
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gtatgctgtc atggtccttt ctggaagttt ctggtgccat ttctgaactg ttacaacttg 2280
tatttccaaa cctggttcat atttatactt tgcaatccaa ataaagataa cccttattcc 2340
ataaaaaaaaa aaaaaaaaaa 2360

```

<210> 267

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(435)

<223> 5' terminal sequence. integrin, beta 2

(antigen cd18 (p95), lymphocyte

function-associated antigen 1; macrophage antigen

1 (mac-1) beta subunit) (ITGB2) gene.

<400> 267

```

aggagtcccc cggtgcccc tcacctgtg gcaagtacat ctctgcgcc gagtgcctga 60

```

agttcgaaaa gggcccctnt ggaagaactg cagcgcgggc tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaaggcca ggacctgcaa ggagagggac tcagag ggct gctgggtggc 180
ctacacgctg gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg 240
agagtgtgtg gcaggcccca acatcgccgc catcgctggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctcctg ctggtcatct ggaaggctc tgatccacct gagcgacctc 360
cgggagttac aggcgttttg agna ggagaa gctcaagtc cagtnggaac aatgattatt 420
ccctttttca agagc 435

<210> 268

<211> 2776

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2776)

<223> integrin, beta 2 (antigen cd18 (p95),
lymphocyte function-associated antigen 1;
macrophage antigen 1 (mac -1) beta subunit) (ITGB2)
gene.

<400> 268

cagggcagac tggtagcaaa gccccacgc ccagccagga gcaccgccgc ggact ccagc 60
acaccgaggg acatgtctgg cctgcgcccc ccactgctcg ccctgggtggg gctgctctcc 120
ctcgggtgctg tcctctctca ggagtgcacg aagttcaagg tcagcagctg ccgggaatgc 180
atcgagtcgg gggccggtg caccgtgtgc cagaagctga acttcacagg gccgggggat 240
cctgactcca ttcgctgcga caccggcca cagc tgctca tgaggggctg tgcggctgac 300
gacatcatgg accccacaag cctcgctgaa acccaggaag accacaatgg gggccagaag 360
cagctgtccc caaaaaagt gacgctttac ctgcgaccag gccaggcagc agcgttcaac 420
gtgaccttcc ggcgggccaa gggctacccc atcgacctgt actatctgat ggacctctcc 480
tactccatgc ttgatgacct caggaatgtc aagaagctag gtggcgacct gctccgggcc 540
ctcaacgaga tcaccgagtc cggccgcatt ggcttcgggt ccttcgtgga caagaccgtg 600
ctgcggttgc tgaacacgca ccctgataag ctgcgaaacc catgccccaa caaggagaaa 660
gagtgccagc ccccgtttgc cttcaggcac gtgtgaagc tgaccaacaa ctcc aaccag 720
tttcagaccg aggtcgggaa gcagctgatt tccggaaacc tggatgcacc cgagggtggg 780
ctggacgcca tgatgcaggt cggcgctgc ccgaggaaa tcggctggcg caacgtcacg 840
cggtctgttg tgtttgccac tgatgacggc ttccatttcg cgggcgacgg aaagctgggc 900
gccatcctga cccccacga cggccgctgt ca cctggagg acaacttgta caaggaggc 960
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tgccggaagg acaacaatc c atcatctgc tcagggctgg gggactgtgt ctgcgggcag 1620
tgctgtgccc acaccagca cgtccccgc aagctgatat acgggcagta ctgcgagtg 1680
gacaccatca actgtgagcg ctacaacggc caggtctgcg gcggccggg gagggggctc 1740
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ggcccccttg ggaagaactg cagcgcgggc tgtcc gggcc tgcagctgtc gaacaacccc 2040
gtgaagggca ggacctgcaa ggagagggac tcagagggct gctgggtggc ctacacgctg 2100

176/292

```

gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg agagtgtgtg 2160
gcaggcccca acatcgccgc catcgtcggg ggcaccgtgg caggcatcgt gctgatcggc 2220
attctcctgc tggatcatctg gaaggctctg atccacctga gcgacctccg ggagtacagg 2280
cgctttgaga aggagaagct caagtcccag tgaacaatg ataatccct tttcaagagc 2340
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ctcttgagga tgtcaccaat taaccagaaa tccagttatt ttccgccctc aaaatgacag 2520
ccatggccgg ccggtgcttc tgggggctcg tcggggggac agctccactc tgactggcac 2580
agtctttgca tggagacttg aggagggctt gaggttggtg aggttaggtg cgtgtttcct 2640
gtgcaagtca ggacatcagt ctg attaaag gtggtgcaa tttatttaca tttaaacttg 2700
tcagggtata aaatgacatc ccattaatta tattgttaat caatcacgtg tatagaaaaa 2760
aaaataaaac ttcaat 2776

```

<210> 269

<211> 449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(449)

<223> 5' terminal sequence. neogenin (chicken)
homolog 1 (NEO1) gene.

<400> 269

```

ccaggaccct gaaggtgcta ccagctcctc ttacttggcc agctcccaag aggaagattc 60
aggccagagt cttcccactg cccatgttcg ccctccac ccattgaaga gttcgcct 120
gccagcaatc ccgctccag gacctccac ctatgatect gcattgcaa gcacaccatt 180
actgtccag caagctctga accatcacat tcaactcagt aagacagcct ccacgggac 240
tctaggaag ggagccggcc tcctatgcca gtggtgttc ccagtgcctc t gaagtgcag 300
ggagaccaca aggtgtttg gaaggattnc gagagtaggt attgaaccag ntgaggttga 360
ncaaagagtt gggccatngg gggagggatt aattgaangg gaccttaaac gtttttnac 420
aacagcttga cggactttta acggggggc 449

```

<210> 270

<211> 5297

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5297)

<223> neogenin (chicken) homolog 1 (NEO1) gene.

<400> 270

```

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cggctgaggc gcgcgggagg gaaggaggca agggctccgc ggcgctgtcg cgctgccgt 120
cactctcggg gaagagattg cggcggagcg gggagcccg cgactcctca gcacccctc 180
cttctggctc tactgcctgc tgctgctcgg gcgcgggccc cgggcgccg cggcggccag 240
gagcggctcc gcgcgcagc cccaggagc cagcattcga acgttactc cattttattt 300
tctggtggag ccggtggata cactctcagt tagaggctct tctgttatat taaactgttc 360
agcatattct gagccttctc caaaaattga atggaaaaa gatggaactt ttttaaactt 420
agtatcagat gatcgacgcc agcttctccc ggatggatct ttatttatca gcaatgtggt 480

```

gcattccaaa cacaataa ac ctgatgaagg ttattatcag tgtgtggcca ctggtgagag 540
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cagggccaat tccacagaat ccgttcgaaa tacccccagc actgacacca tgccagctc 4080
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cttgccagc tcccaagagg aagattcagg ccagagtctt ccca ctgccc atgttcgccc 4200
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5297

```

<210> 271

<211> 389

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(389)

<223> 3' terminal sequence. pou domain, class 2,
transcription factor 2 (POU2F2) gene.

<400> 271

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caggggaatn nttcatnatg gaaaaagaca actgaatgcc ctcaactgaa tgtcttcac 60
ccctcttgcc tgaaatttcc accttcccat aggctgggga gggagtcagt tccagagcag 120
aggaggggtg caggggttag gagggacttg tgagagctag aacttgga aatggcctag 180
cccacccttc aaaggggaaa agaggggagga acaggggatg aaaagttntc cgcagccttc 240
ccttgaactc tcccctgctg ggggagggag gaggttaaag caagaccccc tgcccaggtg 300
gggagagctg ggggccaggg gagaagggga caaatggtag ggacacattc tgtttgagca 360
caatgctaaa aattctgtac atcctttgg
389

```

<210> 272

<211> 2048

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2048)

<223> pou domain, class 2, transcription factor 2
(POU2F2) gene.

<400> 272

179/292

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cgtaacatg agttgggctt ggggcagatg aggctggctg gcggggcggg cagcatggtt 60
cactccagca tgggggctcc agaaataaga atgtctaagc ccctggaggc cgagaagcaa 120
ggtctggact ccccatcaga gcacacagac accgaaagaa atggacca ga cactaatcat 180
cagaaccccc aaaataagac ctccccattc tccgtgtccc caactggccc cagtacaaag 240
atcaaggctg aagacccagc tggcgattca gcccagcag caccctgcc ccctcagccg 300
gccagcctc atctgcccca ggcccaactc atgttgacgg gcagccagct agctggggac 360
atacagcagc tcctccagct ccagca gctg gtgcttgtgc caggccacca cctccagcca 420
ctgtctcagt tcctgtacc gcaggcccag cagagccagc caggcctgct accgacacca 480
aatctattcc agctacctca gcaaacccag ggagctcttc tgacctcca gcccggggc 540
gggcttccca cacagcccc caaatgcttg gagccaccat cccacccga ggagccagct 600
gatctggagg agctggagca attcgccgc accttcaagc aacgcgcag caagctgggc 660
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acaaaagaga aaacaaaaa taatcacaac agaaaccagc tgccccaag gaaccagag 1980
tgaaaaaaca aaaaaaaa caaaaaaca accaaaaaa aaaaaaac tctacccct 2040
ctagagcc 2048

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<210> 273

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 3' terminal sequence. baculoviral iap
repeat-containing 4 (BIRC4) gene.

<400> 273

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ttttctatct ttccaccagc atggaaca at tgattccttt ttcacacaaa acaaattatg 60
tgattgggga gattaactct aatctccaca tttatataca gaaagctcca tttgttaagc 120
ctatctgaaa agaataaaaa atccagatga ttaattcact tacacttaga aattaaatca 180
gtatactatg aatacacatt gtgttcagtt atagtatgat gcttcttatt cttagtctat 240
ggtttcaatt aaataacagt aaaaaaatg gataatacag ctaataccct gaaaaatcaa 300
gaaattcaaa gattatattg ccaactaaaa cactgccatg tacatttttt ttctacttg 360
gtagcaaatg ctaatggaat tcaatcctga ttacttaaag tcagttcaca tcacacattc 420
aatcagggta ataagaacaa cataacatgc ctaccataga gttagatta a ga 472

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<210> 274
<211> 2540
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2540)
<223> baculoviral iap repeat -containing 4 (BIRC4)
gene.

<400> 274
gaaaaggtgg acaagtccta ttttcaagag aagatgactt ttaacagttt tgaaggatct 60
aaaacttgtg tacctgcaga catcaataag gaagaagaat ttgtagaaga gtttaataga 120
ttaaaaaactt ttgctaattt tccaagtggg agtcctgttt cagcatcaac actggcacga 180
gcagggtttc tttatactgg tgaaggagat accgtgcggg gcttt agttg tcatgcagct 240
gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atccccaaat 300
tgcagattta tcaacggctt ttatcttgaa aatagtgcc aagcagctac aaattctggt 360
atccagaatg gtcagtacaa agttgaaaac tatctgggaa gcagagatca ttttgcctta 420
gacaggccat ctgagacaca tgc agactat cttttgagaa ctgggcagggt ttagatata 480
tcagacacca tatacccgag gaacctgcc atgtattgtg aagaagctag attaaagtcc 540
tttcagaact ggccagacta tgctcaccta accccaagag agttagcaag tgctggactc 600
tactacacag gtattggtga ccaagtgcag tgcttttgtt gtggtggaaa actgaaaaat 660
tggaacactt gtgacgtgc ctggtcagaa cacaggcgac actttcctaa ttgcttcttt 720
gtttttggcc ggaatcttaa tattcgaagt gaactctgat ctgtgagttc tgataggaa 780
ttcccaaat caaccaatct tccaagaaat ccattccatgg cagattatga agcacggatc 840
tttacttttg ggacatggat atactcagtt aacaaggagc agc ttgcaag agctggattt 900
tatgctttag gtgaagggtg taaagtaaag tgctttcact gtggaggagg gctaactgat 960
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gagtgtctgg taagaactac tgagaaaaca ccactactaa ctagaagaat tgatgatacc 1140
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attcatagta tactgattta atttctaagt gtaagtgaat taatcatctg gattttttat 1860
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gaaagataga gattgttttt agaggttggt tgttgtgttt taggattctg tccattttct 2040
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gtagaccocg aagggtttta tggaactaa catcagtaac ctaaccccg tgactatcct 2460
gtgctcttcc tagggagctg tgtgttttcc caccaccac ccttccctct gaacaaatgc 2520
ctgagtgtg gggcactttg 2540

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<210> 275
<211> 842
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(842)
<223> 3' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 275
tagaaagata ttttattttt taggaaaaga gccataatta tcttaaa tgt gaaaaaccac 60
atccaataaa ctgatataaa gttttaggaa caagggaata tcttattgtc acgcattcac 120
agtgaacccc attttaatgc aggtccagag ccaactgcag tcctgtccaa tcccataggt 180
acaagggcct ggctcctctt cctgtgtact gcccgacttc ctcactttac tgggtccagc 240
ataaagcaga tgtccactgt cttcct caca tgctgtgatc ttggcttaga ggtaggcaca 300
gtgccgctcc agcagcgagg ggttcgcgtt acttaggaac agcagctctt tttcccttc 360
ttctgtagga gctntctcat gttgaagcca attgttttcc aaataatact gaatacaact 420
ttcaaattcc tttgggttat agttggaaac caggatggga ataaagggat ccagggcac 480
aaatccttcc tttccagca actcctgcgg cagataggct ttccggggct taaagagaga 540
cccagctcgg ctacagaccg acacaatggc gcctccatgc caatcatnct tcatcatttt 600
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gagggttctt cccaangag cattgatgcc accacggcca cctatg ggtg aaacataccc 720
caatgaactt tgctctttag ctctttcagc acaatttcaa actgatctgg tgcgtccctc 780
aaccgtgtta tgcoctgtca aaccacttct ccagaagac tccctttctt aggttttct 840
ct 842

<210> 276
<211> 1608
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1608)
<223> death associated protein 3 (DAP3) gene.

<400> 276
gaattccgcc ggccccaggc agcgtgtgtc ggtgcctag gctggagaac tagtcct cga 60
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ggaccctggg cgttttttac acatggggac ccaggctcgc caaagcattg ctgctcacct 180
agataaccag gttccagttg agagtccgag agctatttcc cgcaccaatg agaatgacct 240
ggccaagcat ggggatcagc acgagggtca gcacta caac atctcccccc aggatttggga 300
gactgtatct ccccatggcc ttctcctcgt ctttgtgatg caggtgaaga cattcagtga 360
agcttgcttg atggttaagga aaccagccct agaacttctg cattacctga aaaacaccag 420
tttgtcttat ccagctatac gatattctct gtatggagag aagggaacag gaaaaaccct 480
aagtctttgc catgttattc atttctgtgc aaaacaggac tggctgatac tacatattcc 540
agatgctcat ctttgggtga aaaattgtcg ggatcttctg cagtccagct acaacaaaca 600
gcgctttgat caacctttag aggtttcaac ctggctgaag aatttcaaaa ctacaaatga 660
gcgcttcttg aaccagataa aagttcaaga gaagtatgtc tggaataaga gagaaa gcac 720
tgagaaaggg agtctcttgg gagaagtggg tgaacagggc ataacacggg tgaggaacgc 780
cacagatgca gttggaattg tgctgaaaga gctaaagagg caaagttctt tgggtatgtt 840
tcacctccta gtggccgtgg atggaatcaa tgctctttgg ggaagaacca ctctgaaaag 900


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agaagataaa agccccgattg cccccgagga atta gcactt gttcacaact tgaggaaaat 960
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ctttaagccc cggaagcct atctgccccca ggagttgctg ggaaaggaag gatttgatgc 1080
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gaaaaaagag ctgctgttcc taagtaacgc gaacccctcg ctgctggagc ggcactgtgc 1260
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tgggattgga caggactgca gttggctctg gacctgcatt aaaatgggtt tcaactgtga 1440
tgcgtagcaa taagatatc ccttgttcct aaaactttat atcagtttat tggatgtggt 1500
ttttcacatt taagataatt atggctcttt tcctaaaaaa taaaatatct ttctaaaaaa 1560
aaaaaaaaa aaaaaaaaaa aaa aaaaaaa aaaaaaaaaa aaaaaaa 1608

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<210> 277

<211> 361

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(361)

<223> 5' terminal sequence. gonadotropin-releasing hormone 1 (leutinizing-releasing hormone) (GNRH1) gene.

<400> 277

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ttagattgca tgctattgta tgtctacagg gcatttgaca gcccaaggnt aaatccaggt 60
gggacggtat ctaatgatgt cctgtccttc actgtccttg ccatcaccag ccacagagat 120
ccaggctttg gggactocca cagcttatcg accag tgttt gatttagttt ttagcctctt 180
tcccatcaaa tgaaaattaa cttggagaca catttcatta gaaaattaga ggcccccttg 240
gctaggaagg catctggtct ggggactaac tactttgaac agtggtgagt cctctctccc 300
acagatgggt cagccagcag taatgctnag ggaagactga agggatcaaa taganaaatg 360
t

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<210> 278

<211> 470

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(470)

<223> gonadotropin-releasing hormone 1 (leutinizing-releasing hormone) (GNRH1) gene.

<400> 278

```

gggatctttt tggctctctg cctctaaaca gaatgaagcc aattcaaaaa ctctagctg 60
gccttattct actgacttgg tgcgtggaag gctgctccag ccagcactgg tcctatggac 120
tgcgccctgg aggaagaga gatgcgaaa atttgattga ttctttcca a gagatagtca 180
aagaggttgg tcaactggca gaaacccaac gcttcgaatg caccacgcac cagccacgtt 240
ctccccctcg agacctgaaa ggagctctgg aaagtctgat tgaagaggaa actgggcaga 300
agaagattta aatccattgg gccagaagga atgaccatta ctaacatgac ttaagtataa 360
ttctgacatt gaaaatttat aacccat taa atacctgtaa atggtatgaa tttcagaaat 420

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ccttacacca agttgcacat attccataat aaagtgcgtg gttgtgaatg

470

<210> 279

<211> 320

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(320)

<223> 3' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 279

ntctaaatat caacagaaac tttatttctc atcggttcag gaacaatcg agggtagatg 60
gaaagaggaa gggagggaaa gagggaggga ggaagaatcc tgcgaaaagg aagggccaga 120
ctgagggaga agaaaaacat gttcggggca aaagggtaat totcaagtgg ggaatgccaa 180
atgaaggggt gcttacatgg gggcacaaaa ttccaaatca gccacagtgg ggtgagggtga 240
gtatgagacg caggtggggt tgaatgaagg aaagttagta ccncttaggg ctacaggacc 300
ctggggttct tctttcag ag 320

<210> 280

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 5' terminal sequence. interleukin 2
receptor, gamma (severe combined immunodeficiency)
(IL2RG) gene.

<400> 280

attcggcaca gggaactttt cggcctggag tgggtgtgtc aagggaactgg ctgagagtct 60
gcagccagac tacagtgaac gactctgcct cgtcagttag attcccccaa aaggaggggc 120
ccttggggag gggcctgggc tncctcatgc aaccagcata gccctactg ggcccccca 180
tggtacaccc taaagcctga aacctgaacc ccantactct gacagaagaa ccccagggtc 240
ctgtagccct aagtggtagt aactttcctt cattcaaccc acctgcgtct tatactcanc 300
tcanccact gttggctgat tttggatttt tgtggcccca tgtaaggaac cctttaattt 360
ggcattnccc aattgagaat taaccttttt gncccaaca tggtttt 407

<210> 281

<211> 1451

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1451)
<223> interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG) gene.

<400> 281
gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttcctgcagc 60
tgcccctgct gggagtggg ctgaacacga caattctgac gcccaatggg aatgaagaca 120
ccacagctga tttcttctcg accactatgc ccactgactc cc tcagtgtt tccactctgc 180
ccctcccaga ggttcagtgt tttgtgttca atgtcgagta catgaattgc acttgggaaca 240
gcagctctga gcccagcct accaacctca ctctgcatta ttggtacaag aactcggata 300
atgataaagt ccagaagtgc agccactatc tattctctga agaaatcaact tctggctgtc 360
agttgcaaaa aaaggagatc cacctctacc aaacatttgt tgttcagctc caggaccac 420
gggaacccag gagacaggcc acacagatgc taaaactgca gaatctggtg atccctggg 480
ctccagagaa cctaacactt cacaactga gtgaatccca gctagaactg aactggaaca 540
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tgataatcat c 1451

<210> 282
<211> 317
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(317)
<223> 3' terminal sequence. death associated protein 3 (DAP3) gene.

<400> 282
atctaacaca acactttaga aagatatttt attttttagg aaaagagcca taattatctt 60
aaatgtgaaa aaccacatcc aataaactga tataaagttt taggnacaag ggaatatctt 120
attgtcacgc attcacagtg aaaccattt taatgcaggt ccagagccaa ctgcagtcc 180
gtccaatccc atagggtaga agggcctggg ctctcttcc tgtgtactgc ccgacttcc 240
catcttactg ggtccagca taaagcagga tgcactgt cttctcaca tgctgtganc 300
ttggncttag gagtag 317

<210> 283
<211> 358
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(358)
<223> 5' terminal sequence. death associated
protein 3 (DAP3) gene.

<400> 283
aggacgggcg ctttggagcc ggccccaggc agcgtgtgtc ggtcgcctag tctggagaac 60
tagtcctcga ctcacgtgca aggatgatgc tgaaaggaat aacaaggcctt atctctagga 120
tcataagtt ggaccctggg cgttttttac acatggggac ccaggctcgn caaagcattg 180
ctgctcacct agataacca ggttcccagt tgagagtccc gagagctatt ttcccgcaac 240
caatgagaat gaccccggcc caagcatggg ggatcancaa ggagggtcaa gcaa tnacaa 300
canttttccc ccaggatatt tgggagaatt gtaattttcc ccattnggcct ttntttcc 358

<210> 284
<211> 416
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(416)
<223> 5' terminal sequence. ptk2 protein tyrosine
kinase 2 (PTK2) gene.

<400> 284
gcacagaagc tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag 60
cagtatgtca tgaccgcct ccagcaagag tacaaaaagc aaatgctgac tgctgctcac 120
gccctggctg tggatgcaa aaacttactc gatgtcattg a ccaagcaag actgaaaatg 180
cttgggcaga cgagaccaca ctgagcctcc cctaggagca cgtcttgcta cctcttttg 240
aagatgttct ctagccttcc accagcagcg agganttaac cctgtgtcct cagtncgcca 300
gcacttacag ctccaacttt tttgaatgac catctggttg aaaaatcttt ctcatataag 360
tttnaaccac atttggattt ggggttcatt ttttgtttg ttttttttc aatcat 416

<210> 285
<211> 3052
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3052)
<223> ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 285
ccggtgtgaa ggccatgagt gattactggg ttgttgaaa gaagtctaac tatgaagtat 60
tagaaaaaga tgttggttta aagcgatttt ttctaagag tttactggat tctgtcaagg 120
ccaaacact aagaaaactg atccaacaaa ctttagaca atttgccaac cttaatagag 180
aagaaagtat tctgaaattc tttgagat cc tgtctccagt ctacagattt gataaggaat 240
gcttcaagtg tgctcttggg tcaagctgga ttatttcagt ggaactggca atcggccag 300

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aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgacttca 360
ctcaagtgcga aaccattcag tattcaaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcagggtgca cccgagcctc tgacagtgcg ggcacccatcc ctaaccattg 480
cggagaatat ggctgaccta atagatgggt actgccggct ggtgaatgga acctgcagct 540
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ccaacagcga aaagcaaggc atgacggacac acgccgtctc tgtgtcag aa acagatgatt 660
atgctgagat tatagatgaa gaagatactt acaccatgcc ctcaaccagg gattatgaga 720
ttcaaaagaa aagaatagaa cttggacgat gtattggaga aggccaattt ggagatgtac 780
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cgggcctggt gaaagctgtc atcgagatgt ccagtaaaat ccagccagcc ccaccagagg 2340
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ctagccttcc accagcagcg aggaattaac cctgtgtcct cagtcgccag cactcacagc 2760
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gatccaaaat gtggcggttt tctaagaatg aaaattatat gtaagctttt aagcatcatg 2940
aagaacaatt tatgttcaca ttaagatacg ttctaaaggg ggatggccaa ggggtgacat 3000
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<210> 286

<211> 377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(377)

<223> 3' terminal sequence. cyclin-dependent
kinase 4 (CDK4) gene.

<400> 286

```
gnataaaaaa ggaccccaaa tataaaggna gggaaaggga caagagggaa catacccctt 60
agtgtagaga aatgggaagg agaaggagaa gcctcaaaag gaggtgggag gggaatgtca 120
ttaaggcagc aaagtaatct ctgtagaaag atggaggagg accctccata gcctcagaga 180
taaaggcaaa gattgccctc tc agtgtcca gaagggaat gggcagcttt tcttccttcc 240
atgggcagcc actccattgc tcaactccgn ttaccttcat ccttatgtag gataagagtn 300
ctgcagagct tcgaaagggc agagattcgc ttgtgtggg ttaaaagtca gcatttccan 360
cagcagcttt tgcttcc 377
```

<210> 287

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 5' terminal sequence. cyclin-dependent
kinase 4 (CDK4) gene.

<400> 287

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catatctgga caaggcacc ccaccaggct tgcagccgaa acgatcaagg atctgatgcg 60
ccagtttcta agaggcctag atttccttca tgccaattgc atcgttcacc gagatctgaa 120
gccagagaac attctggtga caagtgtng aacagtcaag ctggctgact ttngcctggc 180
cagaatctac agctaccaga tggcacttac acccgtggtt gttacactct ggtacc gagg 240
tcccgaagtt cttctngcag tccacatatg caacacctgt gggacatgtg ggagtgttg 300
ctgtatcttt gcagagatgt ttctgcgaaa ncctctcttt ctgtggnaaa ctctgtaagg 360
ccg 363
```

<210> 288

<211> 1443

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1443)

<223> cyclin-dependent kinase 4 (CDK4) gene.

<400> 288

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gccctcccag tttccgcgcg cctctttggc agctggtcac atggtgaggg tgggggtgag 60
ggggcctctc tagcttgccg cctgtgtcta tggtcgggcc ctctgcgtcc agctgctccg 120
gaccgagctc ggggtgatgg ggcgtagga accggctccg gggccccgat aacgggccgc 180
ccccacagca ccccgggctg gcgtgagggt ctcccttgat ctgagaatgg ctacctctcg 240
atatgagcca tggctgaaa ttggtgtcgg tgcctatggg acagtgt aca aggcccgta 300
tccccacagt ggccactttg tggccctcaa gagtgtgaga gtccccaatg gaggaggagg 360
tggaggaggc cttcccatca gcacagtctg tgaggtggct ttactgaggc gactggaggc 420
ttttgagcat cccaatgttg tccggctgat ggacgtctgt gccacatccc gaactgaccg 480
ggagatcaag gtaaccctgg tgttt gagca tgtagaccag gacctaaagg catatctgga 540
caaggcacc ccaccaggct tgccagccga aacgatcaag gatctgatgc gccagtttct 600
aagaggccta gatttccttc atgccaattg catcgttcac cgagatctga agccagagaa 660
cattctggtg acaagtgggtg gaacagtcaa gctggctgac tttggcctgg ccagaatcta 720
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cagctaccag atggcactta caccggtggt tgttacactc tggtagcgag ctcccgaagt 780
tcttctgcag tccacatatg caacacctgt ggacatgtgg agtggttgct gtatctttgc 840
agagatgttt cgtcgaaagc ctctcttctg tggaaactct gaagccgacc agttgggcaa 900
aatctttgac ctgattgggc tgcctccaga ggatgactgg cctcg agatg tatccctgcc 960
ccgtggagcc tttcccccga gagggccccg ccagtgagcag tcggtgtgtac ctgagatgga 1020
ggagtcggga gcacagctgc tgctggaaat gctgactttt aaccacaca agcgaatctc 1080
tgcctttcga gctctgcagc actcttatct acataaggat gaaggtaatc cggagtgcgc 1140
aatggagtggt ctgccatgga aggaagaaaa gctgccattt cccttctgga cactgagagg 1200
gcaatctttg cctttatctc tgaggctatg gagggtcctc ctccatcttt ctacagagat 1260
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ttccatttc tctacactaa ggggtatgtt ccctctgtc cctttcccta cctttatatt 1380
tggggtcctt ttttatagc gaaaaacaaa accaaaagaa awaatggccc tttttttttt 1440
ttt 1443

```

<210> 289

<211> 394

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(394)

<223> 3' terminal sequence. basic transcription
factor 3 (BTF3) gene.

<400> 289

```

ccgcggtgtg tgcgcctaan ctcagngnngn ccacccgaga ccccttgagc accaacccta 60
gtccccgcgc cggcccctna ttcgctccga caagatgaaa gaaaca atca tgaaccaggg 120
aaaactcgcc aaactgcagg cacaagtgcg cattggtggg aaaggaaactg ctgcgagaaa 180
gaagaagggtg gttcatagaa cagccacagc agatgacaaa aaacttcagt tctccttaaa 240
gangttagggt gtaaacata tctctggnat tgaagagggtg aatatgttta caaaccaggg 300
aacagtgtac cactttaaca acc tnaagt tcagggcatc tctgggcagc ggacactttc 360
accattacng gccttgctga gncaaagcag ctgg 394

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<210> 290

<211> 477

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(477)

<223> basic transcription factor 3 (BTF3) gene.

<400> 290

```

atgcgacgga caggcgcacc cgctcaggct gactctcggg ggcgagggtc agccaggggc 60
ggctgccctg gggcgaggc gacgtgtct caacctccac ctgcggcgg aaccgagga 120
gaggagcctc agatgaaaga aacaatcatg aaccag gaaa aactcgccaa actgcaggca 180
caagtgcgca ttggtgggaa agtgaatatg ttacaaacc aaggaaactg gatccacttt 240
aacaacccta aagttcaggc atctctggca gcaaacactt tcaccattac aggccatgct 300
gagacaaagc agctgacaga aatgctaccc agcatcttaa accagcttgg tgcggatagt 360
ctgactagtt taaggagact ggccgaagct ctgcccacac aatctgtgga tggaaaagca 420
ccacttgcta ctggagagga tgatgatgat gaagttccag gaggttcca agaata 477

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<210> 291
 <211> 388
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(388)
 <223> 3' terminal sequence. colony stimulating
 factor 1 receptor, formerly mcdonough feline
 sarcoma viral (v-fms) oncogene homolog (CSF1R)
 gene.

<400> 291
 tgctgttagt ttaatgtgga cagagacatc ccacggcgtg actgttagt t aggatgagtc 60
 agcttggggg agtttgtgct tcctgcttgg nggtggccagc cacatgccaa ggtcccctgc 120
 cttctagccc agaatgacgg gactgggcag aacacccccca acttttagct gccacttggc 180
 tcattacagc agtaccagta tgggggtggg aggggtgagg cnttgagtg aaggcggcgt 240
 atagggcaga gactaagagg gtcctgtg ag attccttagag gagccatcct gntccaagg 300
 gcctgagctg agtntgggtc tgtgagcatc tgctgctcct ctcagagagg ggagatctca 360
 ctctctgccg gtctgtctag ccccaaag 388

<210> 292
 <211> 3992
 <212> DNA/RNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<220>
 <221> misc_feature
 <222> (1)..(3992)
 <223> colony stimulating factor 1 receptor,
 formerly mcdonough feline sarcoma viral (v-fms)
 oncogene homolog (CSF1R) gene.

<400> 292
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 ggagaagaga gaagaggaag aggaagagga agagaggaag cggagggaaac tgcggccagg 120
 ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaacaa gacaaacagc 180
 cagtgcagag gagaggaacg tgtgtccagt gtcccgatcc ctgcggagct agtagctgag 24 0
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 cagatcgtgt gtcagccag cagcgttgat gttaactttg atgtcttcct ccaacacaac 1020

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aacactaagc tcgcaatccc tcaacaatct gactttcata ataaccgtta ccaaaaagtc 1080
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tctttggggc tagacagact ggcagagagt gagatctccc tctctgagag gagcagcaga 3660
tgctcacaga ccacactcag ctccagcccc ttggagcagg atggtcctc taag aatctc 3720
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ccccatact ggtactgctg taatgagcca agtggcagct aaaagttggg ggtgttctgc 3840
ccagtcctgt cattctgggc tagaaggcag gggaccttgg cattggctgg ccacaccaag 3900
caggaagcac aaactcccc aagctgact c atcctaacta acagtcaagc cgtgggatgt 3960
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```

<210> 293

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

191/292

<221> misc_feature

<222> (1)..(356)

<223> 3' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 293

```
tttatttagt caaattatatt tacaacatgg ncttctttga cagttgtcag cttaacactt 60
aatatagtta aaaaagtcaa caattacctg caaaattata tataatnnaa tgtctaaaaa 120
tatgtngctt atatagagca ggaaaatccc tcctctccac aagggaagt ttcgttggtt 180
tncccagagc tgtgattatn gcagtactgt tacacgcatt tccaaagcat taaagancata 240
aatgggatta tctttncctt gcttgtgtat gcctgtnaaa taactgtacc agtggctttg 300
ctttctcata ggtcagtgac ttaaacagcc ctgtttcctt ttcggctata g ggcat 356
```

<210> 294

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(465)

<223> 5' terminal sequence. friend leukemia virus
integration 1 (FLI1) gene.

<400> 294

```
gaccaaagca gtttcttgtc aatacacggg gttcagtatg acacagaatc atggacttaa 60
cccgcatgtg tctggtttga gatttagtga caaatagagg tgggaagctt ataactaat 120
tttaggagga ccaaattcag tggatggcaa ctggaacatt gattgtaagg ccagtgaagt 180
tttcacccaa ctggaatttg atggaaagaa gggt tgtgtg ttttaagacgc caagggcatt 240
gcagaatccc tctcagtgga cagtatgcac tcagctgacc actctctcta gccaatagtc 300
aagatatgga actaaggaaa ttttaatgcc aaattacata cattcctgaa agacggggga 360
attaaattna ctaattttnt tttttttttt ttaaattgatn gacagtggnt ccccggaact 420
tgggaaangt tgtaggggnt ttctaaacc aagncgattc gcant 465
```

<210> 295

<211> 2957

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2957)

<223> friend leukemia virus integrati on 1 (FLI1)
gene.

<400> 295

```
gaattcccaa acgtgcacag gggagtgagg gcagggcgct cgcagggggc acgcaggag 60
ggcccagggc gccaggagg cgcgcgggg ctaatccgaa ggggctgcga ggtcaggctg 120
taaccgggtc aatgtgtgga atattgggg gctcggctgc agacttggcc aatggacgg 180
gactattaag gaggctctgt cggtggtgag cgacgaccag tccctctttg actcagcgta 240
cggagcggca gccatctcc ccaaggccga catgactgcc tcggggagtc ctgactacgg 300
gcagccccac aagatcaacc ccctcccacc acagcaggag tggatcaatc agccagtga 360
ggtcaacgtc aagcgggagt atgaccacat gaatgatcc agggagtctc c ggtggactg 420
```

192/292

```

cagcgtagc aaatgcagca agctggtggg cggaggcgag tccaacccca tgaactacaa 480
cagctatatg gacgagaaga atggccccc tctcccaac atgaccacca acgagaggag 540
agtcacgtgc cccgcagacc ccacactgtg gacacaggag catgtgaggc aatggctgga 600
gtgggccata aaggagtaca gcttgatgga gatcgacaca tctttttcc agaacatgga 660
tggcaaggaa ctgtgtaaaa tgaacaagga ggacttcctc cgcgccacca ccctctacaa 720
cacggaagtg ctgttgcac acctcagtta cctcaggga agttcactgc tggcctataa 780
tacaacctcc cacaccgacc aatcctcacg attgagtgtc aaagaagacc cttcttatga 840
ctcagtcaga agaggagctt ggggcaataa catgaattct ggctcaaca aaagtctctc 900
ccttgagggg gcacaaacga tcagtaagaa tacagagcaa cggccccagc cagatccgta 960
tcagatcctg ggcccagcca gcagtgcct agccaacct ggaagcgggc agatccagct 1020
gtggcaattc ctctggagc tgcctccga cagcgccaac gccagctgt a tcacctgga 1080
ggggaccaac ggggagttca aaatgacgga ccccgatgag gtggccaggc gctggggcga 1140
gcggaaaagc aagcccaaca tgaattacga caagctgagc cgggccctcc gttattacta 1200
tgataaaaac attatgacca aagtgcacgg caaaagatat gcttacaat ttgacttcca 1260
cggcattgcc caggctctgc agc cacatcc gaccgagtcg tccatgtaca agtacccttc 1320
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cgtgccttca cacttaggca gctactacta gaagcttctt ctactgaag cccatcctgc 1560
acacttactg gatgcttttg actcaacagg acatattgtg ccttgaaggg aagacaaaac 1620
tgatgttctt ttctgttg atagaacctt tgtatttgtt ctttaaaaac atttttttta 1680
atgttggtaa cttttgcttc ctctacctga acaaaga gat gaataattcc atgggccagt 1740
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atggttaagt catggttctg agaaagaagc tgtacgtttt ctttatgttt ttatgaccaa 1860
agcagtttct tgtcaatata cggggttcag tatgacacag aatcatggac ttaaccctgc 1920
atgttctggt ttgagattta gtgacaaata gaggtgggaa gcttataatc taattttagg 1980
aggaccaaat tcagcggatg gcaactggaa cattgattgt aaggccagtg aagttttcac 2040
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tccctctcag tggacagtat gcaactcagc gacctctc tctagaaata gtcaagatat 2160
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atcagaaggc aacttactgt ataaa ttatg cagagttatt ttcctatatc tcacagtatt 2400
aaaaataaaa taattaaaaa ttaagaataa ataaacgagt tgacctcgtt cacaaaagca 2460
gttttactat cgaatcaatc gctgttattt ttttttaatg taatttgtac atcttttttc 2520
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cctatagctg aaaaaggaaac agggctgttt aagtcactga cttatgagaa agcaaagcac 2640
tggtacagtt atttaacagg catacacaag cagggaaaag ataatccatt tagatcttta 2700
atgctttgga aatgcgtgta acagtactgc aataatcaca gctctgggaa aaacaacgaa 2760
actttccctt gtggagagga gggattttcc tgcctctata t aagcaacata tttttagaca 2820
ttaaaatata tataattttg caggtaattg ttgacttttt taactatatt aagtgttaag 2880
ctgacaactg tcaaagaaga ccatgttgta aaataatttg actaaataaa tggttccttc 2940
tctcaaaaaa aaaaaaa 2957

```

<210> 296

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 3' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 296

193/292

```

cacccttctt cttcacagat cacgaagatc ccattgaatg gcttgggctg cagacatttc 60
cagtcctgca gtcaatgcct ctctgcccc ccttttggtc agtgtggctg gtgcaganca 120
aatgtgtgcg atcggaggaa tgcctgagcg ggacatggac tcaacagatc tgtctgcctg 180
caatctacaa ggtaggaatc tctaacagct ggcatacatg tttttgtttg gtgttttttt 240
tttttttttg gtttggtttg gtttggtttt tgttttttta gatacaaatc ccactaatga 300
aaaaaattta aaaatcaatt tactcattta ggctgtgagg tcatcaggct aaagcaccat 360
ctctctcttg ggctttatcc ctggggcagg ggagggggg 400

```

<210> 297

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(464)

<223> 5' terminal sequence. ests, highly similar
to tvhume hepatocyte growth factor receptor
precursor [h.sapiens] (EST R97218) gene.

<400> 297

```

cgtggtagat tttcatagtg ccgaatatat gcttaagcaa ataaggcaac acagtttagca 60
tggctgcgat gttagccaat gtccattgcc agaaactgag ttctctatca gcaagagatg 120
tgctcatott gttctggact atatctctc a gggactaga gggcagcctg ctaaattggtta 180
tgcactcaat aaatatTTTT ggaatgaatt aaagagtggc atggcttaca gaagtataga 240
tgtagtata gtatccgtt gagcctttgc ttttttttct gggaacactg aaggaagact 300
cacagccacc catgggtgtt tgaccctcca ctgacctgc ccacctcacc ccgggaaata 360
atcttcagtc tcatctgttg aacagacaag gccacntct atggcttcgg nacaggtagn 420
aaaactgtcc tgtgtggccc cgctnggcag ggatcaccag tttg 464

```

<210> 298

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 298

```

aaataccaaa actacaaaaa tcagtttata aactgttttt ccaaaacaac caccaaaaaca 60
aaacaatccc ccaaatcagg gcaaaacaaa atactgtcaa aagtgttaat cgcccttctc 120
ctaaataaaa agtcattcac actcagccac gtgattggga agagaaaggg ggcttgctct 180
acttgccgac cacatggccg ggtggttccc aagagttagc atggtttatg attttgagaa 240
ccacggaggg ggnaaacagc tgttctgact gcccccctt ttctagacaa ggggtaatat 300
ttcagattca gctagaagag ctttccaat g ttttaagatg atttttaanc cttaatggtt 360
tnaggcctcc ccaacttt 378

```

<210> 299

<211> 317

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(317)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 299

```
actggaagag gttgctcggc gctggggcat ccagaagaac cggccagcca tgaactatga 60
caagctgagc cgctctctcc gctattacta tgaaaagggc atcatgcaga aggtggctgg 120
agagcgatac gtctacaaat ttgtctgtga cccagatgcc ctcttctcca tggctttccc 180
ggataaccag cgtccgttcc tgaaggcaga gtccgagtgc cacctcagcg aggaggacac 240
cctgccgctg acccactttg aagacagccc cgcttacctc ctggacatgg accgctgcag 300
cagcctcccc tatgccg                                     317
```

<210> 300

<211> 4071

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4071)

<223> ets variant gene 5 (ets -related molecule)
(ETV5) gene.

<400> 300

```
gagtccagcc gctggtgcgc ggagcggttc accgtcttcg gagcggttcg gccagcctt 60
tcgcccagcc gccagggccc gctgcgcgcg tgcgtgagcg cgcctgcgcc gccagggccg 120
ctgcaagggg aggagagcgc ccgcctcagg aggatccctt tccccccaga aattactcaa 180
tgctgaaacc tctcaaagtg gtattagaga cgctgaaagc accatggacg ggttttatga 240
tcagcaagtc ccttttatgg tcccagggaa atctcgatct gaggaatgca gagggcggcc 300
tgtgattgac agaaagagga agtttttggg cacagatctg gctcacgatt ctgaagagct 360
atttcaggat ctcaagtcaac ttcaagagcg ttggttagct gaagcacaag ttctgatga 420
tgaacagttt gtcccagatt ttcaagtctga taacctggtg cttcatgccc cacctccaac 480
caagatcaaa cgggagctgc acagcccctc ctctgagctg tcgtcttgta gccatgagca 540
ggctcttggt gctaactatg gagaaaagtg cctctacaac tattgtgcct atgataggaa 600
gcctccctct gggttcaagc cattaacccc tcttacaacc ccctctcac ccacccatca 660
gaatccccta tttccccac ctcaggcaac tctgcccacc tcagggcatg cccctgcagc 720
tgcccaggtt caaggtgtgg gcccgcgcc cgcgcccat tcgcttcag agcctggacc 780
acagcagcaa acatttgcgg tccccgacc accacatcag cccctgcaga tgccaaagat 840
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ccaccccttc cctcctcagc caggagtccc tggagataat cgcccagtt accatcgcca 960
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ccagtaccca atgg gaatca agcaggagcc tcgggattac tgcgtcgatt cagaagtgcc 1140
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cattgcctgg acaggtcgag gcatggagtt caagctgata gaaccggaag aggttgctcg 1440
cgctggtggc atccagaaga accggccagc catgaactat gacaagctga gccgctctct 1500
```

195/292

```

ccgctattac tatgaaaagg gcatcatg ca gaaggtggct ggagagcgat acgtctacaa 1560
atttgtctgt gaccagatg cctctttctc catggctttc ccggataacc agcgtccgtt 1620
cctgaaggca gagtccgagt gccacctcag cgaggaggac accctgccgc tgaccactt 1680
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cattggctgg ggagtgggaa caggaggagg cagaaaacca c caaaaggcc agtgcctcaa 1980
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gtatataaca tgtgtcatgt cctttggaaa cctggtcacc tggtgaaaac ccttgggatt 2940
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aattattctc attgctgtat tatattggaa aagtttttaa caaccaagct aaagctatgt 3180
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gaacctgccg gctgatttga aatactttca ccctgcgcag ggccgtatgc atcctgcca 4020
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```

<210> 301

<211> 407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(407)

<223> 3' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 301

```

nccngtataa aaaaggaccc caaatataaa ggtagggaaa gggacaagag ggaacata cc 60

```

196/292

```

ccttagtgta gagaaatggg aaggagaagg agaagcctca aaaggngagg tgggagggga 120
atgtcattaa ggcagcaaag taatctctgt agaaagatgg aggaggaccc tccatagcct 180
cagagntaaa ggcaaagntt gccctctcag tntcngaag ggaaatggca gcttttcttc 240
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gggtgctgca gagctcgaaa ggcagagat tcgcttntgt ggggttaaaa gtcagccttt 360
nccgcgacga gctttgcttc cccgactcct nccttttcag gnacccc 407

```

<210> 302

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(405)

<223> 5' terminal sequence. cyclin -dependent
kinase 4 (CDK4) gene.

<400> 302

```

attcgnaca gaggaggagg tggaggaggc cttcccatca gcacagttcg tgaggtggct 60
ttactgaggc gactggaggc ttttgagca t cccaatgttg tccggctgat ggacgtctgt 120
gccacatccc gaactgaccg ggagatcaag gtaaccctgg tgtttgagca tgtagaccag 180
gacctaaaga catatctgga caaggcacc ccaccaggct tgccagccga aacgatcaag 240
gatctgatgc gccagtttct aagaggccta gatttccttc atgccaattg catcgttcac 300
cgaggatctg aagccagaga acattctggg tgacaagtgg ttggancagt caagctggct 360
ggactttggg cctgggcagn aatctancag cttaccagat gggca 405

```

<210> 303

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(420)

<223> 3' terminal sequence. v -yes-1 yamaguchi
sarcoma viral oncogene homolog 1 (YES1) gene.

<400> 303

```

caatgagaac tttttatttc aattatccac aaaacaatat tacaatactt tataaaaaata 60
ttaagtttag gctaccatta ttcatttaaa aaagtgtgct agaaggctgt ttttgccaac 120
ttcctttttt ggtaagggtt aacttcaca ttaagacact gaagacgaaa agctgttggt 180
aaaatatctc caaatattaca aagttgtttt tcttgggcaa tttaaaaata cagganfaat 240
ttaaantgaa tacacattaa ggtaggtgt tttatcccta ctatacaatt gttattatat 300
agggaaactgc tcccttcn gg ttaaanccct aatggaatac ccatcaactt ttcccgcccc 360
ntactttccc nggattgggg tttagggtac ctaaacggga aatttaggtc nccccnttg 420

```

<210> 304

<211> 4517

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene
homolog 1 (YES1) gene.

<400> 304

```
gcggagccaa ggcacacggg tctgaccctt gggccggccc ggagcaagtg acacggaccg 60
gtcgccctatc ctgaccacag caaagcggcc cggagcccg cggaggggacc tgacgggggc 120
gtaggcgcgcg gaaggtctggg ggcccggag cgggcccgc gtggcccgag ttccggtgag 180
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```


198/292

```

gttatggcctt cacattcatt gcagtgggat atggttttta tgtaaaacat ttttagaact 3120
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taaaactaat atttttataa a gtattgtaa tattgttttg tggataattg aaataaaaag 4500
ttctcattga atgcacc 4517

```

<210> 305

<211> 459

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(459)

<223> 3' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 305

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ncttgtctga aggtgtgctg gacacctcct ggggctcttc tgggtcattt ggttctggag 60
aattatctct tatctctggc atagagccca agggagagtg gggcatctct tgagggtctt 120
ctttatctct tatttggggg atcagggttg cactggccac ttgcacagtg ctagttagga 180
ggctgggcat ctctctctgag tcttctttcg cattcatttt ggangttaac ttgtcattgg 240
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gggctgggag actcaactcag gatctcatcg ctttgctggg agg atgttcc agggctcact 360
gactcttggg cgcacaaggt gaaacagctt ggtttgaagg gggttnttgg tngggggcaa 420
gcncaatngg gtatggaagg aagcttcctt ctaanaagg 459

```

<210> 306

<211> 370

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

199/292

<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. interferon -induced
protein 75, 52kd (IFI75) gene.

<400> 306
tgcgtttgtc aaagcacaga cttcctgttt tgccgtgctag catctccctg taactctccc 60
aatcttgagg agtgatccct gtccc agccc ctggaaaggg anggaaacga caaactcaaa 120
gtccaggatg ttaccatga caagagccat ggaagaggct ctttttcagc acttcatgca 180
ccagaagctg gggatgcct atgccatata caagccattt ccttctttg aaggcctcct 240
agacaactcc atcatcacta agagaatgta catggaatct ctggaagcct gtagaaattt 300
gatccctgta tccagagtgg tgcacaacat tctacccaa ctgggagagg actttttaac 360
ctgtntctctt 370

<210> 307
<211> 1541
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1541)
<223> interferon-induced protein 75, 52kd (IFI75)
gene.

<400> 307
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tgaacagctt ggttgagtcg cccagcccat ctgaccctgt cctgcctctc cctgcactca 120
tccaggaagg aagaagcact tcagtgaacca atgacaagtt aacatccaaa atgaatgcgg 180
aagaagactc agaagagatg cccagcctcc tcaactagcac tgtgcaagtg gccagtga 240
acctgatccc ccaaataaga gataaagaag acctcaaga gatgcccac tctcccttgg 300
gctctatgcc agagataaga gataattctc cagaaccaa t gacccagaa gagccccagg 360
aggtgtccag cacaccttca gacaagaaag gaaagaaaag aaaaagatgt atctggtcaa 420
ctccaaaaag gagacataag aaaaaagcc tcccaagagg gacagcctca tctagacacg 480
gaatccaaaa gaagctcaaa aggggtggatc aggttcctca aaagaaagat gactcaactt 540
gtaactccac ggtagagaca agggcccaaa aggcgagaa tgaatgtgcc cgaaagtcga 600
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atttaattac cgagattacg gtgagccttt cagggaagcaa tgtggttga cctggttaag 1500
ggaaaggctg attacggaaa tgtacacggg ggcgcggaat t 1541

<210> 308
<211> 416
<212> DNA

200/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(416)

<223> 3' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 308

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ggtannncan tnnatttttt aagagagagg caattttatt cttccaaaaa aatgcaccag 60
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aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tccctgtggc cttggggagg 180
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ggcttcggca acagggcgag acatggccct gtcccttcca cctgagagt c tggggagggg 300
ctggtggcag aaggctccct gcaggagggt cacctgaatg actctcagat tcacagaccc 360
cctnttggcc ccacaacccc tgtaaacatg agaatggggc tcgtgacacc ctnaac 416
```

<210> 309

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(426)

<223> 5' terminal sequence. v-myb avian
myeloblastosis viral oncogene homolog -like 2
(MYBL2) gene.

<400> 309

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cggaccatt caagaaagtc cgaaggtctc tggtcttga cattgtgat gaggatatga 120
agctgatgat gtccacactg ccaaggtctc tatccttgcc gacaactgcc ccttcaaact 180
cttcagcct caccctgtca ggtatcaaag aagacaacag cttgtctaac cagggttct 240
tgcaggccaa gccgagaag gcagcagtgg ccagaagcc ccgaagc cac ttcacgacac 300
ctgccctat gtccagtgc tggaagacg gtggcctgc gggggaccag gggaccagct 360
tttcatggca ggagaaagcc cggcagcttc tggggccgct tgaagcccag ccacactttt 420
cgggac 426
```

<210> 310

<211> 2627

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene
homolog-like 2 (MYBL2) gene.

<400> 310
gctgacgcct tgcagcgcgg ccc gggggccc ggagcggccg gagcagcccg ggtcctgacc 60
ccggcccggc tcccgcctcg ggctctgcgg gcggcggggc gagcgcggcg cggctccgggc 120
cggggggatg tctcggcgga cgcgctgcga ggatctggat gagctgcact accaggacac 180
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cagccacttc cctaaccgca ctgaccagca atgccagtac aggtggctga gagttttgaa 360
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gcctcatctc agacctgct taggatggg gatgtggcca ggggtgctcc tgtgctcacc 2580
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<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth
factor, beta receptor iii (betaglyc an, 300kd)

202/292

(TGFB3) gene.

<400> 311

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cccagactca aggagttggt aaaggggttaa tagccagata gtagaaccag tgaggagatg 60
cggccaaaga ttctttatat ctgaaccaag atgtaaaaca agaatgctt tgaggctttc 120
taagcgatcc tctgtcttaa ttgacactt tgtctggatg cacacttctg accttgctgc 180
cacaacctgt ggggttctga tgtgtccctt gatgggtgct gccctcaggg actgcaccct 240
gacaagtgtt aaggcaacat tcctttcttg tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgtttctt ccatacttg catacaccac tggcaaaatg tcttaatggc 360
aaattttgta ttctttacag ggnctacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggccatt tc 442
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<210> 312

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. transforming growth
factor, beta receptor iii (betaglycan, 300kd)
(TGFB3) gene.

<400> 312

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taacaaggag gtatcactga gcttatttta gctgcaaagt ggcacatat tattccattt 60
aatgaaattc acctcaagcc ctttttgaca tattaaatat atgggatata tttaa ggcaa 120
gagaagtaag gcaatccaaa tgagtgcctt ttccaatct cagcactgtc ttgngngaatt 180
tggtgacact attcagataa ccaactggag accgacagat ttgccatgca ttgcatctt 240
gctagagttt ggtttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta 315
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<210> 313

<211> 4208

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4208)

<223> transforming growth factor, beta receptor
iii (betaglycan, 300kd) (TGFB3) gene.

<400> 313

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gaaagaaccg catgagcctg acggcgcatg gtcttaacat caggctgtgc aggaagaagc 120
tatctgcaga tggatgccag cacacacaag gaagcagagc tctggcaaca ttgagtcaaa 180
gcaaggacac aacatcagag ggacggcaga gaatccttgt gtgtagtctt tgggtggcagt 240
ttgaaaattg caaggaggga cttaagact acttctgatt tgcaaagatg gtctgtgctc 300
cgagcaggct aaagtgactg gacgagacgc actgttgagg aaataaaaat gacttcccat 360
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ggtgactgtg gtgaactgtc acctgtcagt gcctcccatc ctgtccaggc cttgatggag 480
agcttcactg ttttgtcagg ctgtgccagg agaggcaca ctgggctgcc acaggaggtg 540
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203/292

catgtcctga atctcgcact gcgccagggg cctgggcagc tacagagaga ggtcacactt 600
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 gtcaaaaaatc tcatctgat cttgaagtgc aaaaagtctg tcaactgggt gatcaaatct 1200
 tttgatgtta agggaagcct gaaaattatt gtcctaaca gtattggctt tggaaaagag 1260
 agtgaagat ctatgacaat gaccaaatca ataagagatg acattccttc aaccaaggg 1320
 aatctggtga agtgggcttt ggacaatggc tatagtccaa taacttcata cacaatggct 1380
 cctgtggcaa tagtatttca tcttcggctt gaaaataatg aggagatggg agatgaggaa 1440
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 cagaaccgc ccatccgggg aggggaaggc caaatggag gccttcctgt tcttttcca 1560
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 agcgtggata ttgccctgtc tgtcaaatg t gacaatgaga agatgatcgt ggctgtagaa 1740
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 tgcaaggcca agatgaatgg cacacactt gttttggagt ctcctctgaa tggctgcgg 1860
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 cccacaggaa acatcacctt caacatggag ctatacaaca ct gacctctt tttggtgccc 2160
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 aaattctaca gtcccaa gag agtgcacttc cctatccgc aagctgacat ggataagaag 2400
 cgattcagct ttgtcttcaa gcctgtcttc aacacctcac tgctctttct acagtgtgag 2460
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 tcagctcagc tactccaagg gcaggaccaa tggctgagcc tcgtgtccag actcagagg 3000
 ctggattttg gttccctgt aaagacagag tgaatttcag tataaagatc acccgttgta 3060
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 tctatgtgaa acatagcca gtttttaaa tgctgctttg tcca ggtgag aacatccata 3240
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 gtagaaccag tgaggagatg cggccaaaga tcttttatat ctgaaccaag atgtaaaaca 3360
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 gtgtatgcaa gtacaagtat ataatatgtc acctggcaca ttcattttct cagttgaaga 3840
 agagaaaatt tgaaaatgtc cttatgcttt ta gagttgca acttaagtat atttggtagg 3900
 gtgagtggtt ccactcaaaa tatgtcaact taaaaaaa taggccttt cataaaaacc 3960
 aaactgtagc aagatgcaaa tgcatggcaa atctgtcgggt ctccagttgg ttatctgaat 4020
 agtgtacca attccacca gacagtgtg agattggaaa gggcactcat ttggattgcc 4080
 ttacttctct tgccttaaat atatccata tatttaatat gtcaaaaagg gcttgaggtg 4140
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204/292

tccttggt

4208

<210> 314

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(468)

<223> 3' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 314

```
tnnttttttt tttncacctt tccctaatac ttnatnggtn acctctaggc ctgtgtgagg 60
ctgggtgggc ttgggggagg gcgtcactat tcagcttcta ggtggaggca tgagaaggcc 120
ttggctaggc cctccagggt cccatactgt ggagtttgga ggggcaggtc tggcctttcc 180
tggttcagca tagggcacc aggtgggggn acaggtggac acccagcaca ggcacctagg 240
caggggcaca agctcantat ccnttagcca gcctaattgt ntttgg agaa atattccttg 300
ctgtcatcca cgttgggttt aatcgtgtca ctgccagggt tccagccagc gggacaaant 360
ttccccatgt tcgtttgtgt attgggaagg cctggggacca gccgcagagt tnatcccacg 420
gagngtccca aaggnaaatc attaaacagt gattttggcn aaggaaaa 468
```

<210> 315

<211> 394

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(394)

<223> 5' terminal sequence. peroxiredoxin 2
(PRDX2) gene.

<400> 315

```
acttcaaggc cacagcgggt gttgatggcg ctttcaaaga ggtga agctg tcggactaca 60
aagggaagta cgtggctctc tttttctacc ctctggactt cactttttgtg tgccccaccg 120
agatcatcgc gttcagcaac cgtgcagagg acttccgcaa gctgggctgt gaagtgtgtg 180
gcgtctcggg tggactctca gttcacccac ctggcttgga tcaacacccc ccggaagag 240
ggaggcttgg gccccctgaa catc cccctg cttgctgacg tgaccagacg cttgtctgag 300
gattacggcg tgctgaaaac agatgagggc attgctaaca ggggcctctt tatcatcgat 360
gggcaagggt gttcctttcg ccagatcaat gtta 394
```

<210> 316

<211> 937

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

205/292

<221> misc_feature

<222> (1)..(937)

<223> peroxiredoxin 2 (PRDX2) gene.

<400> 316

```
cgcgccccca gggctcactt ggcgctgaga acgcggtgac agcgtgtgat cgtccgtgag 60
tctagccttt gccacgcag ctttcagtca tggcctccgg taacgcg cgc atcggaagc 120
cagccctga cttcaaggcc acagcggtg ttgatggcg cttcaaagag gtgaagctgt 180
cggactacaa agggaagtac gtggtcctct ttttctaccc tctggacttc acttttgtgt 240
gccccaccga gatcatcgcg ttcacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300
aagtgtctgg cgtctcgtg gactc tcagt tcacccacct ggcttggatc aacaccccc 360
ggaaagaggg aggcttgggc ccctgaaca tccccctgct tgctgacgtg accagacgct 420
tgtctgagga ttacggcgtg ctgaaaaacg atgagggcat tgcttacagg ggcctcttta 480
tcatcgatgg caagggtgtc cttcgccaga tcaactgtta tgatttgcct gtgggacgct 540
ccgtggatga ggctctgcgg ctggtccagg cttccagta cacagacgag catggggaag 600
tttgtccggc tgcttgaag cctggacgtg acacgattaa gccgaacgtg gatgacagca 660
aggaatatct ctccaaacac aattaggctg gctaaccgat agtgagcttg tgcccctgcc 720
taggtgcctg tgctgggtgt ccacctgtgc cccacctgg gtgcc ctatg ctgaccagg 780
aaaggccaga cctgcccctc caaaatccac agtatgggac cctggagggc tagcaaggcc 840
ttctcatgcc tccacctaga agctgaatag tgacgcctc cccaagccc accagccgc 900
acacaggcct agaggttaac aataaagtat tagggcc 937
```

<210> 317

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 317

```
gctagcacca tgagctgaag accgagccct ttgatgactt cctgttccca gcatcatcca 60
ggcccagtgg ctctgagaca gccgctccg tggcagacat ggacctatct gggtccttct 120
atgcagcaga ctgggagcct ctgcacagtg gctccctggg gatggggccc atggcacagn 180
agctggagcc cctgtgcact ccggtggtca cctgtactcc cagctgcact gctta cacgt 240
cttcttctgt cttcacctac cccgaggtg actncttccc cagctgtgca gctgcccacc 300
gcaaggcagc agcagcaatg agccttctc tgactcgttc agctnaccca cgggtgctggc 360
cctgtgaggg ggcaggggaa ggggaggcag ncggcaacna caagttgcca ttgtccgagt 420
tngttgattt anagagagga gaaacaaatt t 451
```

<210> 318

<211> 2084

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2084)

<223> v-fos fbj murine osteosarcoma viral oncogene
homolog (FOS) gene.


```

<400> 318
aaccgcatct gcagcgagca actgagaagc caagactgag ccggcgggccg cggcgagcgg 60
aacgagcagt gaccgtgtct ctaccagct ctgcttcaca ggcgccacct gtctccgcc 120
ctcggccctt cgcgcggctt tgcctaaccg ccacgatgat gttctcgggc ttcaacgcag 180
actacgaggc gtcctcctcc cgctgcagca gcgcgtcccc ggccggggat agcctctctt 240
actaccaact acccgagac tccttctcca gcatgggctc gctgtcaac gcgcaggact 300
tctgcacgga cctggccgtc tccagtgcc acttcattcc cagggtcact gccatctcga 360
ccagtcgga cctgcagtgg ctggtgcagc ccgccctcgt ctctctgtg gcccctc gc 420
agaccagagc ccctaccct ttccgagtc ccgccccctc cgtggggct tactccaggg 480
ctggcgttgt gaagaccatg acaggaggcc gagcgagag cattggcagg aggggcaagg 540
tggaacagtt atctccagaa gaagaagaga aaaggagaat ccgaaggga aggaataaga 600
tggctgcagc caaatgccgc aaccggagga gggagc tgac tgatacactc caagcggaga 660
cagaccaact agaagatgag aagtctgctt tgcagaccga gattgccaac ctgctgaagg 720
agaaggaaaa actagagttc atcctggcag ctaccgacc tgctgcaag atccctgatg 780
acctgggctt ccagaagag atgtctgtg cttcccttga tctgactggg ggcctgccag 840
aggttgccac ccg gagtct gaggaggcct tcacctgcc tctctcaat gacctgagc 900
ccaagccctc agtgaacct gtcaagagca tcagcagcat ggagctgaag accgagccct 960
ttgatgactt cctgttccca gcatcatcca ggccagtggt ctctgagaca gcccgctccg 1020
tgccagacat ggacctatct ggtctctct atgcagcaga ctgggagcct ctgca cagtg 1080
gtccctctgg gatggggccc atggccacag agctggagcc cctgtgcaact ccggtggtca 1140
cctgtactcc cagctgcaact gcttacacgt cttccttct cttcacctac cccgaggctg 1200
actccttccc cagctgtgca gctgccacc gcaagggcag cagcagcaat gacccctcct 1260
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ccggcaccga caagtgccac tgcccgagct ggtgcattac agagaggaga aacacatctt 1380
ccctagaggg ttctgtaga cctagggagg accttatctg tgcgtgaac acaccaggct 1440
gtgggcctca aggcattgaa agcatocatg tgtggactca agtccttacc tctccggag 1500
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agtagcatgt tgagccaggc ctgggtctgt gtctctttc tcttctcct tagtcttctc 1620
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aattgtatct agtcagctg attttaacaa taactactgt gtt cctggca atagtgtgtt 1740
ctgattagaa atgaccaata ttatactaag aaaagatacg actttatttt ctggtagata 1800
gaaataaata gctatatcca tgtactgtag tttttcttca acatcaatgt tcattgtaat 1860
gttactgata atgcattggt gagggtgctt gaattgtctg acattaacag ttttccatga 1920
aaacgtttta ttgtgttt tt aatttattta ttaagatgga ttctcagata tttatatttt 1980
tattttattt tttctacct tgaggctctt tgacatgtgg aaagtgaatt tgaatgaaaa 2040
atttaagcat tgtttgctta ttgttccaag acattgtcaa taaa 2084

```

<210> 319

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding protein 7 (RBBP7) gene.

<400> 319

```

ctgcaaaagg aatcaagaag tgttgaagg aaaaagtgtg aaagttatct ttgcatatct 60
gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaggcaa 120
taccctgcta cttgtattta aaatcaatgg tgatgttatt tcttangca cattcttctc 180
ttccctaata gctacaant gatacagtac gcaacagctc acttgaaagt gctagantca 240

```

<210> 320

207/292

<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. retinoblastoma -binding
protein 7 (RBBP7) gene.

<400> 320
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaatat aaa atctggaaga 60
agaatacacc gtttctatat gacctgggta tgacccatgc tcttcagtgg ccagtcctta 120
ccgttcagtg gcttcttgaa gtgactaaac ctgaaggaaa agattatgcc cttcattggc 180
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtgggtgct cgagtacata 240
ttcccaatga tgatgcacag tttgat gctt cccattgtga cagtgacaag ggtgaatttg 300
gtggcttttg ttctgtaaca ggnaaaattg aatgtgaaat taaaatcaat tcacgaagga 360
gaagttaaac cgtgctogtt aacatggccg cagantcctt cacatccatt gcttacaan 420
acaccctctt gcttgatggg gttggnnttt tgactat 457

<210> 321
<211> 1946
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1946)
<223> retinoblastoma -binding protein 7 (RBBP7)
gene.

<400> 321
gcctcgtcag ctgcctgggc gggc tgggag gcgcggggtg aaaagtctcg ttccaagttt 60
ggagagagag agaagagcgc ctgagacctc ggtacccgcg agcggggagg aggcaggaaa 120
gaaggacgcg gcgtctgggg agcaccagg cagcaagacg gggcccgggc tttcgacagt 180
ggggagtgtg acgcgcttgg gaaaggcagg agcgccagg gtcgggctgc tcttggttaa 240
cgagaggagt ccgaggcggc ggcgaggggc gaacgaccg acgcaagatg gcgagtaaag 300
agatgtttga agatactgtg gaggagcgtg tcatcaatga agaataaaa atctggaaga 360
agaatacacc gtttctatat gacctgggta tgacccatgc tcttcagtgg ccagtcctta 420
ccgttcagtg gcttcttgaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480
tagtgctggg gactcatacg tctgatgagc agaatcatct ggtgggtgct cgagtacata 540
ttcccaatga tgatgcacag tttgatgctt cccattgtga cagtgacaag ggtgaatttg 600
gtggcttttg ttctgtaaca ggaaaaattg aatgtgaaat taaaatcaat cacgaaggag 660
aagtaaaccg tgctcgttac atg ccgcaga atcctcacat cattgctaca aaaacaccat 720
cttctgatgt gttgggtttt gactatacaa aacacctgc taaaccagac ccaagtggag 780
aatgtaatcc tgatctcaga ttaagaggtc accagaagga aggcctatgt ctctcctgga 840
attcaaattt gaggggacat ctctaaagt cactgatga ccatactgtt tgcctgtggg 900
atataaacgc aggacaaaaa gaaggcaaaa ttgtggatgc taaaagccatc ttactggcc 960
actcagctgt ttagaggat gtggcctggc acctgctgca cgagtcattg ttggatctg 1020
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gtcacttggg ggatgcgcac actgccgaag tcaactgcct c tcattcaat ccctacagcg 1140
aatatttct agccaccggc tctgcggata agaccgtagc tttatgggat ctgcgtaact 1200
taaaattaaa actccatacc ttgcaatctc ataaagatga aattttccag gtccactggg 1260
ctccacataa tgaaactatt ctggcttcaa gtggtactga ccgccgcctg aatgtgtggg 1320

208/292

```

atttaagtaa aattggggaa gaacaatcag cagaagatgc agaagatggg cctccagaac 1380
tcctgtttat tcatggagga cacactgcta agatttcaga ttttagctgg aaccccaatg 1440
agccttgggt catttgctca gtgtctgagg ataacatcat gcagatatgg caaatggctg 1500
aaaatattta caatgatgaa gagtcagatg tcacgacatc cgaactggag ggaca aggat 1560
cttaaaccca aagtacgaga aatgtttctg ttgaatgtaa tgctacatga atgcttgatt 1620
tatcaagcgc caaaaaggca ttgtatagta ggaaatgtaa gtggggtggc ttatggcttc 1680
tttatcctct gattctagca ctttcaagtg agctgttgcg tactgtatca tattgtagct 1740
attaggaag agaagaatgt tgcttaagaa agaacatcac cattgatttt aaatacaagt 1800
agcagggtat tgcctttgat tcaactgttt taagtctca ttttctcaaa ctaagtgtt 1860
gctgttccca aatatgcaag aataactttt acactttttc cttccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaaat 1946

```

<210> 322

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 322

```

tatagaaatt ctttattatt agacaaaaat agactctctt ttttcccta ttcattgtgat 60
cctactctga atctctgctc agaggaggca gtgactcgct cccaccct ctcccatccc 120
tgccgtgctg gcacctgcag ctgggtggaa ctggcagggg ctgatcccct gggagggctg 180
acgttctcct gcagggtggg ctgcctgac tccttcgggg ctcaactgct gatgcctcct 240
caccctcac acaccatct ctgccatctg ctccatggc aagggtcatc ttgtggggcc 300
tggtccactt taacttaggc agggctgggg ggcgggggaa gggagaggca gtgttcccag 360
gggcc 365

```

<210> 323

<211> 400

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein
(KIAA1075) gene.

<400> 323

```

tcaagggtcg cccagtgag ccctactttg gcagcctgtc cgccttggtc tcccagcact 60
ccatctcccc catctccctg cctgtctgcc tgcgcattcc cagcaaagat cctctggaag 120
agaccccaga ggtccagtg ccaccaaca tgagcacagc gncagacctc ctgcgtcagg 180
gtgtgcctcg caggtngctc tacttgacct cagtggagac agagtactg acgggcccc 240
aagctgtggc ccgggccagc tctgcagctc tgagctgta g cccccgccg acaccagctg 300
ttgtccactt caaggtgtca gccaggga ttnacactga cgggacaacc aaaggaagct 360
ctttnttttc gccgccatta tccagtggaa cagcatcacc 400

```

209/292

<210> 324
<211> 489
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(489)
<223> 5' terminal sequence. atp-binding cassette,
sub-family c (cftr/mrp), member 5 (ABCC5) gene.

<400> 324
nttcggcaca gnaagataca actctgtgct gaacagctgc tgccctgaggc tgacctggcc 60
attcttccca gcagcgacct gacggagatt ggagagcgag tancaacctg agcgggtggc 120
agcgcagagg atcagccttg cccgggcctt gtatagtgc aggagcatct acatcctgga 180
cgacccctc agtgcccttag atgcccattg ggaanccaca tncctcaata gtgctatccg 240
gaaacatctc aagtccaaga cagttctgtt tgttaccac cagt tacagt acctgggttg 300
actgtgatga agtgatcttc atgaaagagg gctgtattta cgggaaagag ggcacccntg 360
gagggaantg atggatttta aatggtgatt atggttacct ttttaattaa cntgtgttg 420
ggggagagac accgccattg agntcatttc aaaaagggga accgtnggtt cacagaggag 480
ttcacagtt 489

<210> 325
<211> 5838
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5838)
<223> atp-binding cassette, sub-family c
(cftr/mrp), member 5 (ABCC5) gene.

<400> 325
ccgggcaggt ggctcatgct cgggagcgtg gttgagcggc tggcgcgggt gtccctggagc 60
aggggcgcag gaattctgat gtgaaactaa cagtctgtga gccctggaac ctccgctcag 120
agaagatgaa ggatatcgac ataggaaaag agtatatcat cccagtcct gggatatagaa 180
gtgtgaggga gagaaccagc acttctggga cgcacagaga ccgtgaagat tccaagtta 240
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<210> 326

<211> 385

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(385)

<223> 3' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 326

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cacacatgta tacactcaaa actacagtga catt ctctac acagnnctat attogatata 180
gcttgaactg ccgaaaaatc angacaatc caaaagggtga ttgcagggtt gatttttttc 240
tccaaaacac ttgaganaca gtaaagctat ttcaacaaag gtcttttctt tgattgtcaa 300
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<210> 327

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(423)

<223> 5' terminal sequence. cadherin 1, type 1,
e-cadherin (epithelial) (CDH1) gene.

<400> 327

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gtttgtgtct ttgtctggcc acatcttgac taggtattgt ctactctgaa gacctttaat 120
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<210> 328

<211> 4828

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)
 (CDH1) gene.

<400> 328

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<210> 329

<211> 471

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(471)

<223> 5' terminal sequence. zinc finger protein
144 (mel-18) (ZNF144) gene.

<400> 329

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<210> 330

<211> 2227

<212> DNA/RNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)
gene.

<400> 330

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actgtcaacg gcgtccctgt gccccctta acttgaggcc agggaccctc tcccttcttc 1260
cagccaagcc tctccactcc ttccactttt tctgggccct tttttccact tcttctactt 1320
tcccagctc tcccacctt gggggg gggg ggcgggtttt ataaataaat atatatatat 1380
atgtacatag gaaaaaccaa atatacatac ttattttcta tggaccaacc agattaattt 1440
aaatgccaca ggaaacaaac tttatgtgtg tgtgtatgtg tggaaaatgg tgttcatttt 1500
ttttgggggg ggtcttgtgt aatttgetgt ttttgggggt gcctggagat gaactggatg 1560
ggccactgga gtctcaataa agctctgcac catectcgtt gtttcccaag gcaggtgggtg 1620
tgttgggggc ccctcagac ccaaagcttt aggcattgatt ccaactggct gcataatagga 1680
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ttttacaaat gcagtttatc cctgggtctg agggcaagt gcagggtgga ggtggcacct 1860
gcactcacct ctcctcttgc agtggaact ttgtgcaaag aatagatagt tctgcctctt 1920
ttttttttt ttcctgtgtg tgtggccttt gcatcattta tcttgtggaa aagaagattc 1980
aggccctgag aggtctcagc tcttgaggga gggctaaggc ttttagcattg tgaagcgtg 2040
caccaccacc aaccttacc tcaccgggga accctacta gcaggactgg tgggtggagt 2100
tcacctgggg cctagagtgg aagtgggggt ggggttaacct cacacaagca cagatcccag 2160
actttgccag aggcaaacag ggaattccgc cgatactgac gggctccagg agt cgtcgcc 2220
acactcg 2227
```

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<210> 331
<211> 254
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(254)
<223> 3' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331
gcataaagag gaaacatggc tttatgtctg acaagaagtt ttgtcctccc caaggcatat 60
ggcatcaagg ctgggctaac ccagtctcat gaccttgtga atccagtcca caaacacaga 120
gacacgcgtg aagacagctg gccagcggga ccttgcgcat actcggttgg ggattataat 180
tccttcagg gacccagcag ttgtgggtaa agcaggcaag tgggccccg tagtcaccct 240
cacaggcccc caca 254

<210> 332
<211> 362
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(362)
<223> 5' terminal sequence. macrophage stimulating
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332
gccatggncc tgggtgctaca cgatggaccc aaggacccca t tcgactact gtgccctgcg 60
acgtgcgct gatgaccagc cgcatcaat cctggacccc ccagaccagg tgcagtttga 120
gaagtgtggc aagaggtgg atcggctgga tcagcggcgt tccaagctgc gctggttggg 180
ggccatccgg gcaactcacc ctggacagtc agcttgogga atcggcaggg ccagcatttc 240
tgcggngngt ctctagtga ggagcagtng atactgactn cccggaagtg cttctcctcc 300
tncatatnc ctctcacggg ctatgaggtg tggttngggc ancctttttc cagaaccac 360
ag 362

<210> 333
<211> 2219
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2219)
<223> macrophage stimulating 1 (hepatocyte growth
factor-like) (MST1) gene.

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<400> 333

```
agccagaagg atgggggtggc tccactcct gctgcttctg actcaatgct taggggtccc 6 0
tgggcagcgc tggccattga atgacttcca agtgctccgg ggcacagagc tacagcacct 120
gctacatgcg gtgggtgccg ggccttggca ggagatgtg gcagatgctg aagagtgtgc 180
tggtcgctgt gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg 240
ttgccaactg ctgccatgga ctcaacactc gcccacacg aggtgcggc gttctgggcg 300
ctgtgacctc ttccagaaga aagactacgt acggacctgc atcatgaaca atggggttgg 360
gtaccggggc accatggcca cgaccgtggg tggcctgccc tgccaggctt ggagccaca 420
gttcccgaat gatcacaagt acacgcccac tctccggaat ggctggaag agaacttctg 480
ccgtaaccct gatggcgac c cggagggtcc ttgggtgctac acaacagacc ctgctgtgcg 540
cttccagagc tggcgcatca aatcctgccg ggaggccgcg tgtgtctggt gcaatggcga 600
ggaataccgc ggcgcggtag accgcacgga gtcaggggcg gagtgcacg cgtgggatct 660
tcagcacccg caccagcacc ccttcgagcc gggcaagtgc ctgcaccaag gtctggacga 720
caactattgc cggaaatcctg acggctccga cgggcatgg tgctacata cggatccgca 780
gatcgagcga gaggttctgt acctcccccg ctgcgggtcc gaggcacagc ccgccaaga 840
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caccactgcg ggcgtacctt gccagcgttg ggacgcga a atccgcac agcaccgatt 960
tacgccagaa aaatacgctg gcaaagacct tcgggagaac ttctgccgga accccgacgg 1020
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gacgcgcgac aagccgcagt tcacgtttac ctccgaaccg catgcacaac tggaggagaa 1260
cttctgccgg aaccagatg gggatagcca tgggccctgg tgctacacga tggaccaag 1320
gaccccatc gactactgtg ccctgcgacg ctgcgtgat gaccagccgc cat caatcct 1380
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cttgcggaat cggcagggcc agcatttctg cggggggtct ctagtgaagg agcagtggat 1560
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tgtgacctg aaccagcgtg tggccctgat ctgcctgccc cctgaatggt atgtggtgcc 1800
tccagggacc aagtgtgaga ttgcaggctg gggtagagacc aaaggtacgg gtaatgacac 1860
agtccataat gtggccttct tgaatgttat ctccaaccag gagtgtaca tcaagcaccg 1920
aggacgtgtg cgggagagtg agatgtgcac tgagggactg ttggccctg tgggggcctg 1980
tgagggtgac tacgggggccc cacttgctctg ctttaccac a actgctggg tcctggaagg 2040
aattataatc cccaaccgag tatgcgcaag gtcccgttg ccagctgtct tcacgcgtgt 2100
ctctgtgttt gtggactgga ttcacaaggc catgagactg ggtagggccc agccttgatg 2160
ccatatgcct tggggaggac aaaacttctt gtcagacata aagccatgtt tcctcttta 2219
```

<210> 334

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(431)

<223> 3' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 334

```
gaaaggaagg caaactctgc ccccc gctca gagtcccccc aaccctcaact gtttcccggt 60
gccattgatg gggaggttca cgtactcagg ggaggccagg naggcntgna gcttggggccg 120
ggcactgagg cgcacacat atgtgagag caggggggaa gcatccaggc agccagggtc 180
agggaccnca tggatcagca gcaagtccag caggttntag tcagcgaagg agntctggtc 240
tcccacaatg aaggtcttgc ctccctggtt ctgggacagc aggtctcaa aaggcttcag 300
```

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ttgcccgggc agtgccttca catagtcac cttgcccgcc tcatagttgg tntagatgag 360
ggagatgtat ttgcagcgga ggtctccac gccgttcatt tcacctgtcc accagggtg 420
nctcctttt t 431

<210> 335

<211> 305

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(305)

<223> 5' terminal sequence. glutathione
s-transferase pi (GSTP1) gene.

<400> 335

nattcgccac aggtcgccac catgccgccc tacaccgtgg tctatttccc agttcgaggc 60
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaagga ggaggtngtg 120
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180
aagtccagg acggagacct naccctgtac cagt ccaata ccactctgcg tcacctgggc 240
cgcacccttg ggctnctatg ggaaggacca gcaggangca gccctggtgg acatngtgaa 300
tgacg 305

<210> 336

<211> 737

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(737)

<223> glutathione s-transferase pi (GSTP1) gene.

<400> 336

ggagtttgc cgccgcagtc ttgccacca tgccgccta caccgtggtc tatttcccag 60
ttcgaggccg ctgcgcggcc ctgcgcatgc tgetggcaga tcagg gccag agctggaagg 120
aggaggtggt gaccgtggag acgtggcagg agggctcact caaagcctcc tgcctatacg 180
ggcagctccc caagtccag gacggagacc tcacctgta ccagtccaat accatcctgc 240
gtcacctggg ccgcaccctt gggctctatg ggaaggacca gcaggaggca gccctggtgg 300
acatggtgaa tgacggcgtg gag gacctcc gctgcaaata catctccctc atctacacca 360
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420
agacctgct gtcccagaac cagggaggca agaccttcat tgtgggagac cagatctcct 480
tcgtgacta caacctgctg gacttgctgc tgatccatga ggtcctagcc cctggctgcc 540
tgatgcgtt cccctgctc tcagcatatg tggggcgcc cagcgcccg cccaagctca 600
aggccttctt ggcctcccct gactacgtga acctcccat caatggcaac gggaaacagt 660
gagggttggg gggactctga gcgggaggca gagtttgcct tcctttctcc aggaccaata 720
aaatttctaa gagagct 737

<210> 337

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(372)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 337

```
gtgggnctgt gttgaaacag gccacgtaaa gcaactctct aaaggtcaaa ccaccataga 60
tttgaatctg ctgggtcattc gccatctgga tttttaactg aatgaatctc atgggtttta 120
ccaaacatgc atgtaatcct gaataccatg anttaaatgc gganttgccc agggacgagg 180
aaaccttcaa gaaacaaggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttggtt gaaacaaagc tcctcagtgg gccagtgaca 300
tccnggggtt ttcttagggt aggctgagga ctgaggggt tatctcacct tctcaggaat 360
gctttttgaa gg 372
```

<210> 338

<211> 508

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(508)

<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 338

```
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tccagtacct taaacctga ttgtgtatat tcatatattt tggatacgca 120
ccccccaact cccaatactg gctctgtctg agtaagaaac agaatcctct ggaacttgag 180
gaagtgaaca tttcggtgac ttccgcatca ggaaggctag agttaccag agcatcaggc 240
cgccacaagt gcctgctttt aggagaccga agtccgcaga acctgectgt gtcccagctt 300
ggaggcctgg gtcctgggaa ctgagccggg gccctcactg gccttccttc caggggatgg 360
atcaacaggg gcagtggtgt cttccgaatg tctgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttaggagggg tttgggtggg gcttggtcac ctgg ggggcc 480
ttccaggtag ggcccttttt aagtggga 508
```

<210> 339

<211> 445

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(445)

<223> 3' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 339

219/292

```
tttttttant caaaagtttg aaattcaagt aactttattt aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaatact tctaggttaa ctagaccaga tctgactt tg gactttattc tttaaacaan 180
ttgcagagan tagagaaaaa antaggttat ttacagaaaa caatatctac atatgtactt 240
ngnggtacaa ntttgggtga cagaaaagac ttcagggtata tgctgggcac cttaggaagn 300
cagttctcaa agggnccttag gttttattnn cttggatttt taaggattgc cctaagganc 360
ccttcttcat cctcgn tctt ggggngggc aggtaggtnt tttaggtgtc ccntatccc 420
ganttttata ctctncaccg ggggg 445
```

<210> 340

<211> 437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(437)

<223> 5' terminal sequence. proliferating cell
nuclear antigen (PCNA) gene.

<400> 340

```
gctccagcgt tgtaaacctg cagagatgga ctctctccac gtctcttttg tgcagctcac 60
cctgcggtct gagggtctcg acacctaccg ctgcgaccgc aacctggcca tggggtgaac 120
ctcaccagta tgtccaaaat actaaaatgc gccggcaatg aagatatcat tacactaagg 180
gccgaagata acgcgggatac cttggcgcta gtatttgaag caccaaacca ggagaaagt 240
tcagactatg aaatgaagtt gatggattta gatgttgaac aacttngaag tccagaacag 300
gagtacagct gtgtagtaaa gatgccntct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacgggagt gaaaattttt 420
ctgcaagtgg gagnact 437
```

<210> 341

<211> 1231

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)
gene.

<400> 341

```
aggtctcagc cggctcgtgc gacgttcgcc cgctcgtctt gaggtctcctg aagccgaaac 60
tagctagact ttcctccttc ccgcctgcct gtagcggcgt tggttgccact ccgccaccat 120
gttcgaggcg cgccgtggtcc agggctccat cctcaagaag gtgttgaggg cactcaagga 180
cctcatcaac gaggcctgct gggatattag ctccagcggg gtaaacctgc agagcatgga 240
ctogtcccac gtctcttttg tgcagctcac cctgcggtct gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggcgtgaa cctcaccagt atgtccaaaa tactaaaatg 360
cgccggcaat gaagatatca ttactaag ggccgaagat aacgcggata ccttggcgct 420
agtatttgaa gcaccaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgaa ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540
tggtgaattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660
```

220/292

```

attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggta cctgaact tc ttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtaccc cttgttgtag agtataaaat 840
tgcggatatg ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg cttctaagat 960
gccagcatat actgaa gtct tttctgtcac caaatttgta cctctaagta catatgtaga 1020
tattgttttc tgtaaataac ctattttttt tctctattct ctccaatttg tttaaagaat 1080
aaagtccaaa gtctgatctg gtctagttaa cctagaagta tttttgtctc ttagaaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg ttttt 1200
gaatttaaat aaagttactt gaatttcaaa c                                1231

```

<210> 342

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(383)

<223> 3' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 342

```

tttttttttt aaacacacan gttttcacgc tgtagtaact tggaaatgtg caaccctgtg 60
caacagagac agaaaagcca aagtaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga ttttacacca aaaatattt c cacaattact tgctctcata 180
ggggtggatc gaagtcttaa aacttgaaaa acaatcaaag aaggttaagt gttctcgggt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggaggggaac gatgatgcca agttactgca taatttaggg tacattgtat ggaatggggg 360
gctactgggg gtactttttt tac                                383

```

<210> 343

<211> 483

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(483)

<223> 5' terminal sequence. adenovirus 5 ela
binding protein (BS69) gene.

<400> 343

```

gttnaaattg cagggactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcatct ttgtcctaac atgagtgtt gtaacaaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg ttaaatgctt cccttccctt occacatata atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgttat gttttagagt aatgggtgca ttgcctaagt gaactccatc actgtacaca 360
gaatgaagga nttaatgcca tgtaatttt cttgttattt aagg atgccg tggatttggt 420
aaaaggctct gtattttgcy gggatgtctg gggttaggga ggccttacct ataggggntg 480
ggg                                483

```

<210> 344
<211> 2722
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(2722)
<223> adenovirus 5 ela binding protein (BS69)
gene.

<400> 344
ggagcataat gctaaagaag taaacaggtc atggcacggt taacaaaaag acgacaggcg 60
atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120
ttgccaaatc tgaccgtatt acaaaatgtg aaacaactac attattcttg aacctatggt 180
gatttttaca tcattacaca gatatgtcat tttcattagt tgtatcattg ttataaaactg 240
gtatatgtct cgagtcacag gtatgcaccc taaagagacc acccgtcagc tgagcttagc 300
tgtgaaaagat ggtcttattg tc gaaactct aacagtgggc tgcaaagggt caaaagctgg 360
tattgaacaa gaaggatatt ggttgccagg agatgagatt gactgggaaa cagaaaatca 420
tgactggtat tgttttgaat gccatttgcc tggagagggt ttgatattgt acctgtgttt 480
tcgtgtgtat cattccaagt gtttgtctga tgagttcagg cttagagaca gcagtagtcc 540
ctggcagtg ccagtttgca ggagcattaa gaagaagaat acaaacaaac aggagatggg 600
cacatacctc agattcattg tctcccgcag gaaggagagg gctatagatc ttaataaaaa 660
ggggaaggac aataaacacc cgatgtacag gaggctgggt cactcagctg tggacgttcc 720
caccattcaa gagaagtgat atgaaggga ataccgaagt ta tgaagagt tcaaagctga 780
tgcccaattg cttctccaca ataccgtgat tttctatgga gcagacagt agcaagctga 840
cattgcgagg atgctatata aagacacatg tcatgagctg gatgaactgc agctttgcaa 900
gaattgcttt tacttgtcaa atgctogtcc tgacaactgg ttctgttatc cttgtatacc 960
taatcatgag ctggtttggg ctaaaatgaa aggttttggg ttttggccag ccaaagtcac 1020
gcagaagaag gacaatcaag tcgacgttcg cttctttggc caccaccacc agagggcctg 1080
gattccttct gaaaacattc aagatatcac agtcaacatt catcggtcgc acgtgaagcg 1140
cagtatgggt tggaaaaagg cctgtgatga gctggagctg catcagcgtt tcctacgaga 1200
aggagattt tggaaatcta agaagagga ccgagggtgag gaagaggcag aatccagtat 1260
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acgtaatcaa agtgtggagc ccaaaaagga agaaccagag cctgaaacag aagcagtaag 1380
ttctagccag gaaataccca cgatgcctca gccc atcgaa aaagtctccg tgtcaactca 1440
gacaaagaag ttaagtgcct cttaccaag aatgctgcat cggagcacc agaccacaaa 1500
cgacggcgtg tgtcagagca tgtgccatga caaatacacc aagatcttca atgacttcaa 1560
agaccggatg aagtcggacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620
gaagctgctg tctgaaatgg aagaagaaaa gagacaagct gtaaataaag ctgtagccaa 1680
catgcagggt gagatggaca gaaaatgtaa gcaagtaaag gaaaagtgtg aggaggaatt 1740
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gaagcagtggt tgctacaact gtgaggagga ggccatgtac cactgctg ct ggaacacatc 1860
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agcgggtttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgcaccag 2040
cctttaaaca cttttcgtga ag aaattttg cacagtagtt taaatctttt gttaatgctc 2100
ctccgaagtt tttcagggg taaaagtaac atcagtggag ggtattattt taaataaatt 2160
ttaattgaga atttgttgca ttttcagcaa attttaaac atttttagggt tttacagaga 2220
ttttaacctt taaacaacag atctttaaaa aacagggtgaa tacaagttag ttttaacaaag 2 280
aaacatttag aatagatctg aatgtaagaa tctcagaact gtttcagaaa taaaacatac 2340
taccttgatg tgacattttt ttcttaacct tggtgagctg gttttgttca gcttaattta 2400
ctgttcaaag gcattatctg ttgttcacac cagtgggtat atgattgaat ttagggaaca 2460
gggttgacac agcagggcta gtctgcata tttttt ctta aatatttccc aattgtgttt 2520
ttcattatct cttttcaata tataactttt ataacaaatt attagctttg atctttagt 2580
ttaaaattgc agggaactgg ggtaatcttt tactgagctg gatccttagag aaaatgaata 2640
tttaaatatt aaagtttgcc acatttcac tttgtcctaa catgagtgtc tgtaacaaaa 2700

222/292

taaaacaaca aaaacaaagc ct

2722

<210> 345

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(363)

<223> 3' terminal sequence. matrix
metalloproteinase 11 (stromelysin 3) (MMP11) gene.

<400> 345

```
gcattgcagca tcctgagtgg tagcgtcgat ctacagagggc acccctctcc agtcagtggc 60
cctgcgggna cggngactgt ctacacgccg ggtgctgggg tggaacgcc agtagtcctt 120
gcctcggaag aagtagatct tgttcttctc gggacccag accaaggc ag catggaccgg 180
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggactgg cttttcaccg 240
tcgtacaccc agtacttgag caccttgga agaaccacaaat gtgggcccgg cttaccagc 300
attggccttt tcgccacagg gctggggcag tccctgccag tngcgagaag ccaattttgg 360
gca                                     363
```

<210> 346

<211> 2260

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2260)

<223> matrix metalloproteinase 11 (stromelysin 3)
(MMP11) gene.

<400> 346

```
aagcccagca gcccggggc ggatggctcc ggccgcctgg ctccgcagcg cgccgcgcgc 60
cgccctcctg ccccgatgc tgctgctgct gctccagccg ccgcgcgtgc tggcccgggc 120
tctgccgccc gacgtccacc acctccatgc cgagaggagg gggccacagc cctggcatgc 180
agccctgccc agtagcccgg cacctgcccc tgccacgcag gaagcccccc ggccctgccag 240
cagcctcagg cctccccgct gtggcgtgcc cgacccatct gatgggctga gtgcccgcaa 300
ccgacagaag aggttcgtgc tttctggcgg gcgctgggag aagacggacc tcacctacag 360
gacccctcgg ttcccatggc agttggtgca ggagcaggtg cggcagacga tggcaga ggc 420
cctaaaggta tggagcgatg tgacgccact cacctttact gaggtgcacg agggccgtgc 480
tgacatcatg atcgacttgc ccaggtactg gcatggggac gacctgccgt ttgatgggcc 540
tgggggcctc ctggcccacg ccttcttccc caagactcac cgagaagggg atgtccactt 600
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcagggtggc 660
agcccagtaa tttggccacg tgctggggct gcagcacaca acagcagcca aggccctgat 720
gtccgccttc tacaccttc gctaccactc agtctcagc ccagatgact gcaggggcgt 780
tcaacaccta tatggccagc cctggcccac tgtcacctcc aggaccccag cctggggccc 840
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900
ctgtgaggcc tcctttgacg cggctctccac catccgaggc gagctctttt tcttcaaagc 960
gggctttgtg tggcgctcc gtgggggcca gctgcagccc ggctaccag cattggcctc 1020
tcgccactgg cagggactgc ccagccctgt ggacgtgcc ttcgaggatg ccca gggcca 1080
catttggttc ttcaaagggt ctcagtactg ggtgtacgac ggtgaaaagc cagtcctggg 1140
```

223/292

```

ccccgcaccc ctcaccgagc tgggcctggt gaggttcccc gtccatgctg ccttggtctg 1200
gggtcccgag aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccaccc 1260
cagcaccggg cgtgtagaca gtcccgtgc c ccgcagggcc actgactgga gaggggtgcc 1320
ctctgagatc gacgctgcct tccaggatgc tgatggctat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaaggt gaaggctctg gaaggcttcc cccgtctcgt 1440
gggtcctgac ttctttgggt gtgccgagcc tgccaacact ttcctctgac catggcttgg 1500
atgccctcag ggggtgctgac ccctgccagg ccaogaatat caggctagag acccatggcc 1560
atctttgtgg ctgtgggcac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
gggtggggtag aaccaccatg acaactgccg ggagggccac gcaggctcgtg gtcacctgcc 1680
agcgactgtc tcagactggg cagggaggct ttggcatgac tt aagaggaa gggcagtctt 1740
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gtagcaccat ggcaggactg ggggaactgg agtgccttg ctgtatccct gttgtgaggt 1860
tccttcaggg ggctggcact gaagcaaggg tgctggggcc ccatggcctt cagccctggc 1920
tgagcaactg ggctgta ggg cagggccact tcctgaggtc aggtcttggg aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc aggccaaaaa 2040
gttcacagtc aaatggggag ggtattctt catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatcctgtc ccaggccgga tcctcctgaa gcccttttcg cagcac tgct 2160
atcctccaaa gccattgtaa atgtgtgtac agtgtgtata aaccttcttc ttcttttttt 2220
tttttaaaact gaggattgtc attaaacaca gttgttttct 2260

```

<210> 347

<211> 273

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(273)

<223> 3' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 347

```

atgtttattg aacgtaacag tataattcat gtatgttccc ataatttttt catgtactaa 60
ctcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcaatt 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaaagggtg tgttacgaat 180
catcgggggt gtggccagnt tgctcacgg aggtgcagg aggtggggc ctcactaggg 240
canctggagg agcacggact gccctgccg cag 273

```

<210> 348

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(330)

<223> 5' terminal sequence. hypothetical protein
mgc13071 (MGC13071) gene.

<400> 348

```

ggagtacaga acattgtggt aggggaaggg actcactttc tcatcccatg tgtacaaaaa 60
ccaattatct ttgactgctg ttctcaacca cgtagtcgnc cagtcacac tggtagcaaa 120
gatttacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180

```

224/292

```

cctcgcatct tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc tttgatgctg gagaactaat caccagaggg 300
gagcttggtt tccagccngg tgaagnacca                               330

```

<210> 349

<211> 1168

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prime r

<220>

<221> misc_feature

<222> (1)..(1168)

<223> hypothetical protein mgc13071 (MGC13071)
gene.

<400> 349

```

aaatgatgat agtagtacct acagtatagt gctgttagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcaggtg tgagagggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtcctat cggcaagttt ggcctggcct tagctgttgc aggaggcatg gtgacctctg 180
ccttatgtaa tgtggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtac 240
agaacattgt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tctttgactg ctgtttctcaa ccacgtagtg cgccagtcac c actggtagc aaagatttac 360
agaatgtcaa catcacactg tgcacacctt tccggcccat cactagccag cttcctcgca 420
tcttcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tcttcaagtc actggtggct cgctttgatg ctggagaact aatcaccag agggagctgg 540
tctccagcca ggtgagcaac aaccttatgg agtgagcagc cacctttggg ctcattctgg 600
acgacgtgtc tttgacacat ctgaccttct tgaaggagt aacagacagg tggcccccca 660
ggaagcagag agcgccagat ttgtggtgga aaaggcggcc atcatctctg ctgagggtga 720
ctccaaggca gctgagctga tcgccaactc actggccact gcaggggacg gccagagcga 7 80
gctgtgcaag ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgcctg ccggcagggc agtccgtgct cctccagctg ccctagttag gccccagcct 900
acctgcacct ccgtgaggca actgggccac agccccgatg attcgttaaca ccacctttcg 960
ccctcacccc agaaatcact gaaatttcat gattggctta aagtgaagga agtaaaggta 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacggt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                               1168

```

<210> 350

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(315)

<223> 5' terminal sequence. interleukin enhancer
binding factor 2, 45kd (ILF2) gene.

<400> 350

```

ctggctttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
cccaatcttc gaaaactgga tccagaactc catttgata tcaaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctggttc gaggaataatg cttctcagtc cacagttaaa 180
gttcnccanc agantactga aggacttgag gattcgtttt ccnggctttg agc cctcaca 240

```

225/292

```

ccnnggatnc ttgaactact aggnccattat gctgtgatga acaacccccac caganagcct 300
ttggcnctaa acgtt                                     315

```

```

<210> 351
<211> 1552
<212> DNA/RNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(1552)
<223> interleukin enhancer binding factor 2, 45kd
      (ILF2) gene.

```

```

<400> 351
cggttggtgc ggctccatt gttcgtgttt taaggcgcca tgaggggtga cagaggccgt 60
ggtcgtggtg ggcgctttgg ttccagagga ggcccaggag gag gggtcag gccctttgta 120
ccacatatcc catttgactt ctatttgtgt gaaatggcct tccccgggt caagccagca 180
cctgatgaaa ctctcttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240
tctgctgaac aggcattctat ctttctctg gtgacaaaaa taaacaatgt gattgataat 300
ctgattgtgg ctccagggac a ttgaagtg caaattgaag aagttcgaca ggtgggatcc 360
tataaaaagg ggacaatgac tacaggacac aatgtggctg acctgggtgg gatactcaag 420
attctgccaa cgttggaagc tgttgctgcc ctggggaaca aagtcgtgga aagcctaaga 480
gcacaggatc cttctgaagt ttttaaccatg ctgaccaacg aaactggctt tgaaatcagt 540
tcttctgatg ctacagtga gattctcatt acaacagtgc cacccaatct tcgaaaactg 600
gatccagaac tccatttgga tatcaaagta ttgcagagtg ccttagcagc catccgacat 660
gcccgctggt tcgaggaaaa tgcttctcag tccacagtta aagttctcat cagactactg 720
aaggacttga ggattcgttt tcttggtctt gagccccctc c acctggat ccttgacct 780
ctaggccatt atgctgtgat gaacaacccc accagacagc ctttgccctt aaacgttgca 840
tacaggcgct gcttgcatg tctggctgca ggactgttc tgccagggtc agtgggtatc 900
actgaccctt gtgagagtgg caactttaga gtacacacag tcatgacctt agaacagcag 960
gacatggtct gctatacagc tcagactctc gtccgaatcc tctcatatgg tggctttagg 1020
aagatccttg gccaggaggg tgatgccagc tatcttgctt ctgaaatctc tacctgggat 1080
ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaagga 1140
gaggaagaag aggagaatac agaaagaacc acctcaagga gaggaagaag aaagcatgg a 1200
aactcaggag tgacattccc ttcactcctt ttctacccta agggaaagac tggagcctaa 1260
gctgcctgct actggcttta catggtgaca gacattccgt ggataggaag atagcaggag 1320
aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagtctccca 1380
tttgtgacct atgccatcca tctataatgg agg ataccaa catttcttcc taatattcta 1440
taatctccaa ctctgaaaaa cccctctctc aactaatact ttgctgttga aatgtttgtga 1500
aatgttaagt gtctggaaat ttttttttct aagaaaaact attaaagtac tt 1552

```

```

<210> 352
<211> 396
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(396)
<223> 3' terminal sequence. hypothetical protein
      flj11307 (FLJ11307) gene.

```

226/292

<400> 352

```
ctccattaca gggtttttgc cacttgctgt gaggataggg ccctgagttc ttacctctaa 60
ggtactggag gtttc agttg tagaatttcc agtattattg cttgagtttg aagacactgt 120
ttcattttta ctttcattat ctgatttttc atcggaactc atacattcaa tatctgcatc 180
aaagcctgtt ggatatccca ttgcctgcaa taccttcacc gctacgtgaa agttttgctg 240
ttttcttgga tggctcctgag gcttcatatg ttgtgccatc cacatctaca gacattg tga 300
agactggggg catgaacggg ggccagactg aagataagaa gctatactga agcacaggcc 360
tgatctgaat taagcntcat tagtggcatt ccataa 396
```

<210> 353

<211> 1858

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(1858)

<223> hypothetical protein flj11307 (FLJ11307)
gene.

<400> 353

```
tcgatgaaag atcctccgga cttattggac aggcagaaat gcccgaacgc cttggcgtct 60
cttcgacatg ccaaattggtt tcaggcaagg gcaaattgat taaaatcatg tgtaat tgtc 120
ctccgatttc tgctgatttt gtgcaacaga gtcccacatc gggcaccatt gaaaggatgg 180
ccactagaac ttatatgtga aaagtctata ggtacttgta atagaccttt gggcgctggg 240
gaggccttga gacgagtaat ggagtgtttg gcatctggaa tactacttcc tgggggtcct 300
ggtcttcatg atccttgtga gcgagacca acag atgctc tgagctatat gaccatccag 360
caaaaaagaag atattaccca cagtgcacag catgcaactc gactatcagc ctttgccag 420
atttacaagg tgcctggagat ggacccctt ccatctagta agccttttca gaagtattcc 480
tggtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540
ggattagggg atgataaaga cccaacaag aagatgaaac gaaacttaag gaaaattctg 600
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg 660
cttcagtata agctcctatc tcagtctggc cccgttcatg cccagctctt cacaatgtct 720
gtagatgtgg atggcacaac atatgaagcc tcaggacatc ccaagaaaac agca aaactt 780
cacgtagcgg tgaagggtatt gcaggcaatg ggatatccaa caggccttga tgcagatatt 840
gaatgtatga gttccgatga aaaatcagat aatgaaagta aaaatgaaac agtgtcttca 900
aactcaagca ataatactgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960
actcagggcc ctatcctcac agcaagtggc aa aaacctg taatggagct caatgaaaaa 1020
agaagaggtc tcaagtatga actcatctca gagactggtg gaagccatga caagcgttt 1080
gtaatggagg tagaagtaga tggacagaaa ttcagaggcg caggctcaaa taagaaagt 1140
gcaaaggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200
aataataaga aaaagaagat tatccctcag gcaaaggcg ttgtgaatac agctgtgtct 1260
gcagcagtc aagctgttcg gggcagagga agagggaactc taacaagggg agcttttgtt 1320
ggggcgacag ctgctcctgg ctacatagct ccaggctatg gaacaccata tggttacagc 1380
acagctgccc ctgcctatgg ttaccctaag agaatggttc tgttac ccgt tatgaaattt 1440
ccaacatata ctgttcccca ctactcattc ttttagcaaa tgacagaagc taattcctat 1500
tgaacaacaa tacagtacaa cacagaatgt tagagaaaaa gcctttttat cctgtcttct 1560
ttgaacacat acttgatcaa aattatttgt aaagaacatc tttcctactt tttgatttta 1620
acaaatgcaa atttagttct ctaaaacttg aaaaaaaaaa aagaaaccag ttctgtgaaa 1680
acgtacctc atttctggaa aataacttat accagccctt ctgttctagg gaaataaaag 1740
tctagcagtt caaagtttaa gttttaagag acgtatcaga ttatgtaaaa ttaattttgt 1800
gaagatgta tagagtctca aacactgac acaataaac tgctttgtt taacacag 1858
```

<210> 354

<211> 242

<212> DNA

227/292

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(242)

<223> 5' terminal sequence. v-myb avian

myeloblastosis viral oncogene homolog (MYB) gen e.

<400> 354

```
agaaccccag ctatcaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacgggtcccc tgaagatgct acctcagaca 120
ccctctcadc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttgctg agtttcaacg aaaatggacc acccttactg aacgaaaatc ntacaacgag 240
gt                                         242
```

<210> 355

<211> 3225

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene

homolog (MYB) gene.

<400> 355

```
ggcggcagcg ccctgccgac gccggggagg gacgcaggca ggcggcgggc agcggggaggc 60
ggcaccgccg tgctccccgc ggctctcggc ggagccccgc cgcccgccgc gccatggccc 120
gaaagaccgc gcacagcata tatagcagtg acgaggatga tgaggacttt gagatgtgtg 180
accatgacta tgatgggctg cttcccaagt ctggaaagcg tcacttgggg aaaacaagggt 240
ggaccgggga agaggatgaa aaactgaaga agctgggtgga acagaatgga acagatgact 300
ggaaagtatt tgccaattat ctccgaatc gaacagatgt gcagtgccag caccgat ggc 360
agaaagtact aaaccctgag ctcatcaagg gtccctggac caaagaagaa gatcagagag 420
tgatagagct tgtacagaaa tacgggtccga aacgttggtc tgttattgcc aagcacttaa 480
agggggagaat tggaaaacaa tgtagggaga ggtggcataa ccacttgaat ccagaagtta 540
agaaaacctc ctggacagaa gaggaagaca gaatt attta ccaggcacac aagagactgg 600
ggaacagatg ggcagaaaatc gcaaagctac tgcctggacg aactgataat gctatcaaga 660
accactggaa ttctacaatg cgtcggaagg tgcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttcagaa gaacagtcac ttgatgggtt 780
ttgctcaggc tccgcctaca gctcaactcc ctgccactgg ccagcccact gttaacaacg 840
actattccta ttaccacatt tctgaagcac aaaatgtctc cagtcatggt ccataccctg 900
tagcggttaca tgtaaatata gtcaatgtcc ctccagcagc tgccgcagcc attcagagac 960
actataatga tgaagaccct gagaaggaaa agcgaataaa ggaattagaa ttgct cctaa 1020
tgtcaaccga gaatgagcta aaaggacagc aggtgtctacc aacacagaac cacacatgca 1080
gctaccccggt gtggcacagc accaccattg ccgaccacac cagacctcat ggagacagtg 1140
cacctgtttc ctgttttgga gaacaccact ccactccatc tctgccagcg gatcctggct 1200
ccctacctga agaaagcgcc tcgccagcaa ggtgcatgat cgtccaccag ggcaccattc 1260
tgataatgt taagaacctc ttagaatttg cagaaacact ccaatttata gattctttct 1320
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ccctcattgg tcacaaattg actgttacaa caccatttca tagagaccag actgtgaaaa 1440
ctcaaaagga aaatactgtt tttagaacct cagctatcaa aaggtcaatc ttagaaagct 1500
ctccaagaac tcctacacca ttcaaacatg cacttgacgc tcaagaaatt aaatacggtc 1560
ccctgaagat gctacctcag acaccctctc atctagtaga agatctgcag gatgtgatca 1620
```

228/292

```

aacaggaatc tgatgaatct ggatttgttg ctgagtttca aga aaatgga ccacccttac 1680
tgaagaaaat caaacaagag gtggaatctc caactgataa atcaggaaac ttcttctgct 1740
cacaccactg ggaaggggac agtctgaata cccaactgtt cacgcagacc tcgcctgtgc 1800
gagatgcacc gaatatctct acaagctccg ttttaatggc accagcatca gaagatgaag 1860
acaatgttct caaagcat tt acagtaccta aaaacaggtc cctggcgagc cccttgacgc 1920
cttgtagcag tacctgggaa cctgcatact gtggaagat ggaggagcag atgacatctt 1980
ccagtcaagc tcgtaaatac gtgaatgcac tctcagcccg gacgctggtc atgtgagaca 2040
tttccagaaa agcattatgg ttttcagaac agttcaagtt gacttgggat atatcat tcc 2100
tcaacatgaa acttttcatg aatgggagaa gaacctatct ttgttgtggt acaacagttg 2160
agagcacgac caagtgcatt tagttgaatg aagtcttctt ggatttcacc caactaaaag 2220
gatttttaaa aataaataac agtcttacct aaattattag gtaatgaatt gtagccagtt 2280
gttaatatct taatgcagat ttttttaaaa aaaaacataa aatgatattat ctggtatttt 2340
aaaggatcca acagatcagt attttttctt gtgatgggtt ttttgaaatt tgacacatta 2400
aaaggtactc cagtatttca cttttctcga tcactaaaca tatgcatata tttttaaaaa 2460
tcagtataag cattactcta agttagact taataccatg tgacatttaa tccagattgt 2520
aaatgctcat ttatggttaa tgacattgaa ggtacattta ttgtaccaa ccattttatg 2580
agttttctgt tagcttgctt taaaaattat tactgtaaga aatagtttta taaaaaatta 2640
tatttttatt cagtaattta attttgtaa tgccaaatga aaaacgtttt ttgctgctat 2700
ggtcttagcc tgtagacatg ctgctagtat cagaggggca gtaga gcttg gacagaaaga 2760
aaagaaactt ggtgttaggt aattgactat gcaotagtat ttcagacttt ttaattttat 2820
atatatatac atttttttct cttctgcaat acatttgaaa acttgtttgg gagactctgc 2880
attttttatt ttggtttttt tgttattggt ggtttataca agcatgcgtt gcacttcttt 2940
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ataatttggg agttctcgat ttgatccgca tcccctgtgg tttctaagtg tatggtctca 3060
gaactgttgc atggatcctg tgttgcaac tggggagaca gaaactgtgg ttgatagcca 3120
gtcactgcct taagaacatt tgatgcaaga tggccagcac tgaacttttg agatatgac g 3180
gtgtacttac tgccttgtag caaaataaag atgtgccctt atttt 3225

```

<210> 356

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(369)

<223> 3' terminal sequence. zinc finger protein 9
(a cellular retroviral nucleic acid binding
protein) (ZNF9) gene.

<400> 356

```

gtagttaa at gcagaaagtc ggtttttttc caccctttc ctctttttac acggcaagta 60
aagctcactg gcttgggagt tgcctctatc tgccaacctt tggccagtga agaggattca 1 20
gagaaaataa tacaaccatc aatcagaaaa aggaggggag acaaaggaaa ataattaggc 180
tgtagctcaa ttgtgcatc cgtgcaagg tggcctgact cgccacagcg gtaacagttg 240
acttcacttg tcttgcctga gttgatggct acatgaccag tttcaccaca cctatagcac 300
ttcacttttg tgcagtcttt tttgaatgtg tcccgaattc tcccacaaga atancctttc 360
tgctcanct 369

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<210> 357

<211> 1500

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1500)
<223> zinc finger protein 9 (a cellular retroviral
nucleic acid binding protein) (ZNF9) gene.

<400> 357
gaattccaaa cagcctctac cttgcgagcc gtcttcccca ggctgcgtc cgagtctcgc 60
ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120
ttcaagtgtg gacgatctgg ccactgggccc cgggaatgtc ctactggtgg aggccgtggt 180
cgtggaatga gaagccgtgg cagagggtgt tttacctcgg atagagggtt ccagtttggt 240
tctcgtcttc ttccagatat ttgttatcgc tgtggtgagt ctgggtcatct tgccaaggat 300
tgtgatcttc aggaggatgc ctgtataaac tgcggtagag gtg gccacat tgccaaggac 360
tgcaaggagc ccaagagaga gcgagagcaa tgcgtctaca actgtggcaa accaggccat 420
ctggctcgtg actgcgacca tgcatatgag cagaaatgct attcttggtg agaattcgga 480
cacattcaaa aagactgcac caaagtgaag tgctataggt gtggtgaaac tggcatgta 540
gccatcaact gcagcaagac a agtgaagtc aactgttacc gctgtggcga gtcagggcac 600
cttgacggg aatgcacaat tgaggctaca gcctaattat tttcctttgt cgccctcct 660
ttttctgatt gatggttgta ttattttctc tgaatcctct tcaactggcca aaggttgga 720
gatagaggca actcccaggc cagtgaagct tacttgccgt gtaaaaggag gaaaggggtg 780
gaaaaaaacc gactttctgc atttaactac aaaaaaagt tatgtttagt ttggtagagg 840
tgttatgtat aatgctttgt taaagaaccc cttttccgtg ccactggtga atagggattg 900
atgaatggga agagttgagt cagaccagta agcccgctc gggttccttg aacatgttcc 960
catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020
ttagtataat gatggtcttg gattgtctga cctcagtagc tattaataa catcaagtaa 1080
catctgtatc aggccttaca tagaacatac agttgagtgg gagtaacaa aaagataaac 1140
atgcgtgtta atggctgttc gagagaaatc ggaataaaag cctaaacagg aacaacttca 1200
tcacagtgtt gatgtt ggac acatagatgg tgatggcaaa ggtttagaac acattatatt 1260
caaagactaa atctaaaacc cagagtaaac atcaatgctc agagtttagc taatttgagg 1320
ctattcagga attgcagaga aatgcatttt cacagaaatc aagatgttat tttgtatatac 1380
tatatcactt agacaactgt gtttcatttg ctgtaatcag tttttaaag tcaga tggaa 1440
agagcaactg aagtcttaga aaatagaaat gtaattttaa actattccaa taaagctgga 1500

<210> 358
<211> 425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(425)
<223> 3' terminal sequence. camp responsive
element modulator (CREM) gene.

<400> 358
ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaactg tagtaaatgt 60
tcagatattt aaatgagcac caaacactac aaagtgcac caacatggtt ctattaaaaa 120
ctcnccttga ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180
actaatataa aaatctgcaa atgcatataa ttcatatcta ggctattctt cncatatagg 240
catgtcatta gatagacttt ctttctatcc ttccngagg natttttttg nggtttacnt 300
ttattgnact gctggatgca ttatttttga tcatcctttc ctaaaatgnt ttaaagacct 360
gcaataaatt ttattg cata ggacacnatt ggtgncacat agaatgggag cngcaagtat 420
gtggc 425

<210> 359

230/292

<211> 232
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(232)
<223> 5' terminal sequence. camp responsive
element modulator (CREM) gene.

<400> 359
ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60
agcttttctt gttagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120
gaaacacgtc atgaaactgt aatgcatgaa cagaactcag gagttgtctg gccagcttag 180
tgctgccact ggtgacatgc caacttacca gatccgagct cctantgnng ct 232

<210> 360
<211> 1431
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:prime r

<220>
<221> misc_feature
<222> (1)..(1431)
<223> camp responsive element modulator (CREM)
gene.

<400> 360
atgaccatgg aaacagttga atcccagcat gatggaagta taacagcttc tttgacagag 60
agcaagtctg ctcatgtgca gactcagact gggcaaattt caatccctgc tttagctcag 120
tgcaagtgagc tgagatcagg caccagaaga ggctcccag ctgtaactct agtgcaagta 180
ccttcggggc aaactataca tgtccaggga gtaattcaga caccacagcc atgggttatt 240
cagtcacatcag aaatacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300
gaatcagaag gtgtaattga ttctcataaa cgtagagaaa t cctttcacg aagaccctct 360
tataggaaaa tactgaatga actgtcctct gatgtgcctg gtgttcccaa gattgaagaa 420
gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480
atatatcaga ctagcacggg gcaatacatt gctatagccc aagggtggaac aatccagatt 540
tctaaccagc gatctgatgg tggttcaggga ctgcaggcat taacaatgac aaattcagga 600
gctcctccac caggtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660
cagttctttg tcccaggcag ccagggtgtt gttcaagctg ccaactggtga catgccaaact 720
taccagatcc gagctcctac tgctgctttg ccacaggag tggtgatggc tgcacgccc 780
ggaagtgtgc acagtcccca gcagctggca gaagaagcaa cagcgaacg agagctgagg 840
ctaataaaaa acagagaagc tgcccgggag tgcgcagga agaagaaaga atatgtcaaa 900
tgtcttgaaa atcgtgtggc tgtgcttgaa aaccaaaca agactctcat tgaggaaactc 960
aaggccctca aagatcttta ttgccataaa gtagagtaac tgtctttgac ttggaccttg 1020
tttactctaa tcaaggcagg agatgcagca gtccacttta ttgccatgtg gacttgtggg 1080
aaggacacgt gtgaccctta agaatccagt ttggattagt gtttgaaatt gaattgggaa 1140
tgttgttcca ggaatgtgaa tgcagcgtga tcacacttac cgagcttact ttgatctgtt 1200
tgtcaatagc atgcataaaa tgcttgttt gccctttgct tctgcttttt ttcagggaag 1260
ctgccaaaaga atgtcgacgt cgaaagaaag aatatgtaaa atgcctggag agccgagttg 1320
cagtgctgga agtccagaac aagaagctta tagaggaact tgaaacctg aaagacattt 1380
gttctcccaa aactgattac tagaaatatt taactatgaa ctgattacag a 1431

231/292

<210> 361
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 3' terminal sequence. cathepsin b (CTSB)
gene.

<400> 361
caagttggag aaacctttaa ttggcacagg cattccttgt taacttgaca gggatgaagct 60
gtaatttttc aaaaacagta aaagctggtt tctcctaaac tattttcctt gtggtagtag 120
agatcagtgg gtcagaaaca actcctgacc acttggtttc cttttgagcc gcgtcattag 180
gaggcaatct gtaaaactag cacaggtctc ccgctgttcc actggctcac ccacatg att 240
agcagagtgc acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300
gaggttgtga cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360
agggctccca acaccatctc tcctctgatt tctgtgacaa atgtggaagc tacttgcttg 420
gaggtagtgg gggaactgat gggggaactt tcac cg 457

<210> 362
<211> 401
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(401)
<223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362
atcatgcatt gcaacattta ttgatggagt tttcccaatt taatatttct catcatttcc 60
tcacatgatt agtactgcta gcggacctac taaaatttta acactgactt attattagag 120
atggcttgca tttttcctac accattccaa aggagaacat tagatgtctg tattaaattc 180
aagcaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgt g gcncttaagg 240
tgaataagggt ggtggtgact gttctgcaga gagtttctca taagcaggty gagcattggg 300
aaccacagggt tcacagtttt tctcttgaag agacactttg ctgtcccgat gatcaaacc 360
ttcttgaggg catcttcctg ttaaggcaca ttgaggccaa c 401

<210> 363
<211> 370
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(370)
<223> 5' terminal sequence. melan -a (MLANA) gene.

232/292

<400> 363

```
attaaggaag gtgtcctgtg ccctgaccct acaagatgcc aagagaagat gctcacttca 6 0
tctatggtta cccaagaag gggcacggcc actcttacac cacggctgaa gaggccgctg 120
ggatcgcat cctgacagt atcctgggag tcttactgct catcggtgt tggatttga 180
gaagacgaaa tggatacaga gccttgatgg ataaaagtct tcatgttggc actcaatgtg 240
cttaacaaga agatgccac aagaagggtt tgatcatcgg gacagcaaag tgtctcttca 300
agagaaaaac tgtgaacctg tggttcccaa tgcctccact gcttatggag aaactctctg 360
cagaacagtc                                     370
```

<210> 364

<211> 1524

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1524)

<223> melan-a (MLANA) gene.

<400> 364

```
agcagacaga ggactctcat taaggaaggt gtcctgtgcc ctgaccctac aagatgcca 60
gagaagatgc tcaattcatc tatggttacc ccaagaagg gacggccac tcttacacca 120
cggctgaaga ggccgtggg atcggcatcc tgacagtgat cctgggagtc ttactgctca 180
tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240
atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggtt gatcatcggg 300
acagcaaatg gtctcttcaa gagaaaaact gtgaacctgt ggttccc aat gctccacctg 360
cttatgagaa actctctgca gaacagtcac caccacctta ttcacctta gagccagcga 420
gacacctgag acatgctgaa attatttctc tcacactttt gcttgaattt aatacagaca 480
tctaattgtt tcctttggaa tgggttagga aaaatgcaag ccatctctaa taataagtca 540
gtgttaaaat ttagtaggt ccgct agcag tactaatcat gtgaggaaat gatgagaaat 600
attaatttg gaaaactcca tcaataaatg ttgcaatgca tgatactatc tgtgccagag 660
gtaattgttg taaatccatg gtgttatatt ctgagagaca gaattcaagt gggattctg 720
gggccatcca atttctctt acttgaaatt tggctaataa caaactagtc aggttttcga 780
accttgaccg acatgaactg tacacagaat tgttccagta ctatggagt ctcacaaagg 840
atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgct 900
agcaatgtct ctttgtgctc taaaattcta ttatactaca ataatatatt gtaaatatcc 960
tatagctctt tttttttgag atggagtttc gcttttgttg cccag gctgg agtgcaatgg 1020
cgcgatcttg gctcaccata acctccgct cccaggttca agcaattctc ctgccttagc 1080
ctcctgagta gctgggatta caggcgtgcg ccactatgcc tgactaat ttt tgtagt tttta 1140
gtagagacgg ggtttctcca tgttggtcag gctggtctca aactcctgac ctcaggtgat 1200
ctgcccgcct cagcctccca aagtgctgga attacaggc tgagccacca cgctggctg 1260
gatcctatat cttaggtaag acatataacg cagtctaatt acatttctact tcaaggctca 1320
atgctattct aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380
aataagtaaa agctactatg tactgcctta gtgctgatgc ctgtgtactg ccttaaatg t 1440
acctatggca atttagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500
aatcataaag gatcagagat tctg                                     1524
```

<210> 365

<211> 556

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

233/292

<221> misc_feature
<222> (1)..(556)
<223> 3' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 365
actattcggtt aggccttttat ttttctctat gttctgcagt aactaaggaa aatcatggta 60
aatgtcaatc ttcacacaac agcagacaca aagggtttca gaaacgtcag atatgaag aa 120
atctccatc cttcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180
ctataagtgc tgtacaagat catagattat gatggaacga cttcatttta gaacgttagc 240
aaaactgtta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300
ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa ttttccatta 360
tcaaaaagca aacactctat ttgcagttg aacaatgatc actgatcaca aatatacnaat 420
acagtgtccc ccgcccccaa tcgacatcat tttccactta gggaccctgg catccactcc 480
ctgggggtac ccgtgactcc ncctttacac cccccagggg ctggcctcag atctacctaa 540
gggnggggat aacc cc 556

<210> 366
<211> 464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(464)
<223> 5' terminal sequence. apr -1 protein (APR-1)
gene.

<400> 366
aacagcgcca aggaagctct ggtctggaaa gtgctgggga agttaggaat gcagcctgga 60
cgtcagcaca gcatcttttg agatccgaag aagatcgtca cagaagagtt tgtgcgcaga 120
gggtacctga ttataaaacc ggtgccccgt agcagtcagg tggagtatga gttcttctgg 180
gggccccgag cacacg tgga atcgagcaaa ctgaaagtca tgcattttgt ggcaagggtt 240
cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcggga cgatgatgca 300
gaggttgagg ctatcctcaa ttcagggtgct aggggttatt ccgcccccta agtagatctg 360
gaggcagacc cttggggggt gtaaaagaga gtnacaggta cccccaaagg agtagatg nc 420
aaggggccct aagttgcaaa atgatgtcga ttttggggcc gggg 464

<210> 367
<211> 1476
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1476)
<223> apr-1 protein (APR-1) gene.

<400> 367
ctggaagaat tcgcgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcggggct 60
tgcagctgcg gcaagtgcgt gcggcggctg ctgcgcgaag tcagctggcg tgggaactac 120
cctttgtagc tgagaacggc ttgtttattg ctacaaagac totattgaca ttggtagctt 180
cagcggcagc agcttct tac ggtataaagc tggtgcttcc tgaagaggct acaagcatcc 240

234/292

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ttccctagga ctgctgtaag ctttgagcct ctagcaggag acatgcctcg gggacgaaag 300
agtgcggcgc gccgtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccctatggcc gcctctgtgg tagcgagcac ccccgaaga c 420
gacctgagcg gccccgagga agaccgagc actccagagg aggctctac caccctgaa 480
gaagcctcga gcaactgcca agcacaaaag ctttcagtgc cccggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcatcatggg caacagcgcc 600
aaggaagctc tggcttgga agtgctggg aagttag gaa tgcagcctgg acgtcagcac 660
agcatctttg gagatccgaa gaagatcgtc acagaagagt ttgtgcgcag agggtagctg 720
atttataaac cgggtgcccc tagcagtcgc gtggagtatg agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccga 840
tgctctaaag actggccttg taattatgac tgggattcgg acgatgatgc agaggttgag 900
gctatcctca attcagggtc taggggttat tccgcccctt aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtag cccaaggagt agatgccagg gtcctaagtt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgtgat cagtga tcat 1080
tggtcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttaaaa 1140
ttcgtttgtg tgagaataac aatatgttta aaaatataat tgaacaaatt tttttctttg 1200
tttctgtca ttgacattta gtataacagt tttgctaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaaataag ctgttctttt gaagttgaaa 1320
taccagtaaa aatgttgaag aaggatggag gatttcttca tatctgacgt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttcctta gttacttgac 1440
gtcttgtatc tctttttatt ttcggattgc ttatca 1476

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<210> 368

<211> 436

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(436)

<223> 3' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 368

```

cgtttttttg ctttaataac caaaactaca aaaatcagtt tataaactgt ttttccaaaa 60
caaccaccaa aacaaaacaa tcccccaaat cagggcaaaa caaaatactg tcaaaagtgt 120
taatcgccct tctcctaaaa taaaagtcac ccacactcag ccacgtgatt ggaagagaa 180
agggggcttg ctctacttgg cgaccacatg gccgggtggg tcccaa gagt agccatgggt 240
tatgatattg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caaggggtaa tatttcagat tcagctagaa gagctttcca atgtttaaga tgtattttta 360
acccttaatg gtttgagcct cccaactta gcctacttac tttcnaagg gtttgtgatt 420
tttcaacaaa ttgtgc 436

```

<210> 369

<211> 414

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(414)

<223> 5' terminal sequence. ets variant gene 5
(ets-related molecule) (ETV5) gene.

<400> 369
ggttgctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60
ccgctctctc cgctattact atgaaaaggg catcatgcag aaggtggctg gagagcgata 120
cgtctacaaa ttgtctctgtg acccagatgc cctcttctcc atggctttcc cggataacca 180
gcgtccgttc ctgaaggcag agtccgagtg ccacctcagc gaggaggaca ccctgccgct 240
gaccacattt gaagacagcc ccgcttacct cctggacatg gaccgctgca gcagcctccc 300
ctatgccgaa ggtttgctta ctaagtttct gagtggcgga gtgnccaaac cctaggagct 360
agcagttccc attcagggca aacaagnngc agtgngttt gtt ttgtgtt tttt 414

<210> 370

<211> 249

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(249)

<223> 5' terminal sequence. cd69 antigen (p60,
early t-cell activation antigen) (CD69) gene.

<400> 370

ataataagga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60
tcagtggatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120
atagtgtctt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180
aaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240
cccngacgc 249

<210> 371

<211> 1702

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1702)

<223> cd69 antigen (p60, early t-cell activation
antigen) (CD69) gene.

<400> 371

agactcaaca agagctccag caaagaacttt cactgtagct tgacttgacc tgagattaac 60
tagggaatct tgagaataaa gatgagctct gaaaattgtt tcgtagcaga gaacagct ct 120
ttgcatccgg agagtggaca agaaaatgat gccaccagtc ccattttctc aacacgtcat 180
gaagggctct tccaagttcc tgtcctgtgt gctgtaatga atgtggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaatata attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccattgttct tcatgc tctg aggactgggt tggtaccag 360
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
tctgaacatg gtgctactct tgcgtgcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgag gtagagagga aactggggtt ggactgaaaa aggaacctgg tcacctatgg 540
aagtgggtcaa atggcaaaga atttaacaac tggttcaacg ttacagggtc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtgatgctg ctctgtggtc cgaagtcttc cataga gact 780

236/292

```

ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagAAC tatggaaaaa 840
aaggaaagaaa ttccaggaaa atctgcactg tgggctttta ttgccatgag ctagaagcat 900
cacaggttga ccaataacca tgcccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaa ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggtg ctagatactg aatgtaaaca aaggaattat ggctggtaac atagggtttt 1140
agtctaattg aatcccttaa actcaggag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatatttctc tctttttaga gaaatttgcc aatttacttt gttatttttc 1260
cccaaaaaag atgggatgat cgtgtattta ttttttact tctcagctg tagacaggtc 1320
cttttcgatg gtacatatat ctttgccttt ataacttttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aa                                     1702

```

<210> 372

<211> 585

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(585)

<223> 3' terminal sequence. oncogene tc21 (TC21) gene.

<400> 372

```

gtaggcagta tgattccaaa agttaaaaaat tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaac tgattcatct ctattaaaaat gtaagcactt aaaaaaagag 120
catgtctgtg tatatagaca tat atttttaa aggaatcaga taatctttga agcagcctta 180
gtgtttcctt taaatttgtc tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatggtga tcatttgtct aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcttt tcttgccgt tggtagctaa 360
aactgaaggg attctagaaa atgacacaaat ggcagccttt cntgtctttt tctttccgtg 420
ttggttcngg tgaaggagga cattcctggc cctggaaatt tccnggataa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc oggatgcnc catgtatgtt 540
acctaagctg ccggcaacgg tngcctctnc cggggtaccg gcc ng                                     585

```

<210> 373

<211> 451

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(451)

<223> 5' terminal sequence. oncogene tc21 (TC21) gene.

<400> 373

```

gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60

```

237/292

```
acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gagttcccaa tgattt taat tggtaataaa 240
gcagatctgg atcatcaaag acaggtaaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcacagca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttatt aggaaatttc aagancagga atgtcctctt cacagaccac 420
acggaaaaga aagccagaaa gctg cattgt g 451
```

<210> 374

<211> 425

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 374

```
gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctctga 60
caaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atatttcaaa 120
aacacagata aatagtttac tacagataaa tagcttcacc c tttggtgtc ctcccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca cccaacccc 240
caacctcagt ggaaagcaat gcccagggat taggctatgg aaggggcaaaa tggaccatt 300
caaatttcct cccagggacc aggccttatt aaccctggga aatgtcctta gctggtgggg 360
gaaagggttg cgattcagga atacatatgt gtagtttttg ttagaagcca tccatagcac 420
acccg 425
```

<210> 375

<211> 478

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing
function and indian blood group system) (CD44)
gene.

<400> 375

```
ggcgttccag ttcccacttg gaggcenntc atccctcggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttctgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aatagggcct ggtccctggg aggaaatttg aatgggtoca ttttgccctt 180
ccatagccta atccctgggc attgctttcc actgaggttg ggggttgggg tgtactagtt 240
acacatcttc aacagacccc ctctangaaa tttttcagat gcttctggga gacacccaaa 300
ggggaagct atttactgt agtaaaactat ttatctgtgt ttttgaaata ttaaaccttg 360
gatcagtcct ttgatcagta taaatTTTTT aaagttaactt ttgtcagagg caccaaagg 420
tttaaaactga ttcataaata aatatcngga cttcctcgat cttccaaaaa aaaaaaaa 478
```


238/292

<210> 376
 <211> 1794
 <212> DNA/RNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:primer
 <220>
 <221> misc_feature
 <222> (1)..(1794)
 <223> cd44 antigen (homing function and indian blood group system) (CD44) gene.

<400> 376
 cccgcgcct ccgttcgctc cggacacccat ggacaagttt tgggtggcag ca gcctgggg 60
 actctgcctc gtgccgctga gcctggcgca gatcgatttg aatataacct gccgctttgc 120
 aggtgtattc cacgtggaga aaaatggctg ctacagcatc tctcggacgg aggccgctga 180
 cctctgcaag gctttcaata gcaccttgcc cacaatggcc cagatggaga aagctctgag 240
 catcggattt gagacctgca ggtatgggtt c atagaaggg catgtgggtga ttccccggat 300
 ccacccaac tccatctgtg cagcaaacaa cacaggggtg tacatcctca catacaacac 360
 ctccccatg gacacatat tcttcaatgc ttcagctcca cctgaagaag attgtacatc 420
 agtcacagac ctgccccatg cctttgatgg accaattacc ataactattg ttaaccgtga 480
 tggcaccgcg tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540
 caacctact gatgatgacg tgagcagcgg ctccctccagt gaaaggagca gcacttcagg 600
 aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660
 gatcaccgac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720
 tgggggggtcc cataccactc atggatctga atcagatgga cactcacatg ggagtcaaga 780
 aggtggagca aacacaacct ctggtcctat aaggacaccc caaattccag aatggctgat 840
 catcttgcca tccctcttgg ccttggtctt gattcttgca gtttgcatg cagtcaacag 900
 tcgaagaagg tgtgggcaga agaaaaagct agtgatcaac agtggcaatg gagctgtgga 960
 ggacagaaag ccaagtggac tcaacggaga gccagcaag tctcaggaaa tgggtgcat 1020
 ggtgaacaag gactcgtcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080
 cctgcagaat gtggacatga agattgggtg gtaacaccta caccattatc ttggaaagaa 1140
 acaaccgttg gaaacataac cattacaggg agctgggaca cttaacagat gcaatgtgct 1200
 actgattgtt tcattgogaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260
 tgttttggtc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320
 cccaattaat aatcagcaag aatttgatcg ttcagttcca cttg gaggcc ttcacccctg 1380
 ggtgtgctat ggatggcttc taacaaaaac tacacatatg tttcctgat cgccaacctt 1440
 tccccacca gtaaggaca tttcccaggg ttaatagggc ctggtccctg ggaggaaatt 1500
 tgaatgggtc cattttgccc ttccatagcc taatccctgg gcattgcttt ccaactgaggt 1560
 tgggtgtgac tagttacac a tcttcaacag accccctcta gaaatttttc agatgcttct 1620
 gggagacacc aaagggtgaa gctatttatc ttagtaaac tatttatctg tgtttttgaa 1680
 atattaaacc ctggatcagt cctttgatca gtataattt ttaaagttac tttgtcagag 1740
 gcacaaaagg gtttaaaactg attcataata aatatctgta cttcttcgat cttc 1794

<210> 377
 <211> 452
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:primer
 <220>
 <221> misc_feature
 <222> (1)..(452)
 <223> 3' terminal sequence. cyclin -dependent kinase inhibitor 3 (cdk2 -associated dual specificity phosphatase) (CDKN3) gene.

<400> 377

```

ttttgtcaat aaaacttttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctgggtggttt cattttcaata caaattatgc tagagaactg acatttcaga catgggtcata 120
tatatgctat ttgaattcct ttatcttcga tacagatctt gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgc cccgaaactc atgaagataa ttgtattgct tgatgggtctg 240
tattgccccg gatcctctta ggtctcgag gctgtctatg gcttgctctg gtgatattgt 300
gtcagacagg tatagtagga gacaagcagc tacaagacaa gatctcccaa gtcctccata 360
gcagtgtatt aagggttttc cggtaatttt t aaggcaggt tgtaagcnc tccattattt 420
cacagcagct ggccatgctn ggagtcctcc ca 452

```

<210> 378

<211> 472

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(472)

<223> 5' terminal sequence. cyclin -dependent
kinase inhibitor 3 (cdk2 -associated dual
specificity phosphatase) (CDKN3) gene.

<400> 378

```

ggcagcagcg gcaactggtc tcgacgtggg gcgccanga ctgaagccca ngnttcaata 60
caaacaagtg agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggctatcttt gtcacgagtg aattgttctc agtttctcgg ttatgtgct 180
cttccaggtt gtaaatttaa agatgttaga agaaatgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acatatttgt tttctgcacc agaggggaac tgtcaaaata 300
tagagtccca aaccttctgg atctctacca gcaatgtgga attatcacc atcatcatcc 360
aatccgcaga tggagggact cctgacatag ccagctgctg tgaaataatg gaagagctta 420
caacctgcct taaaaattac cgaaaaacct taatacactg ctatggagga ct 472

```

<210> 379

<211> 639

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(639)

<223> cyclin-dependent kinase inhibitor 3
(cdk2-associated dual specificity phosphatase)
(CDKN3) gene.

<400> 379

```

atggagccgc ccagttca at acaacaagtg gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgttct 120
cagtttctcg gtttatgtgc tcttccaggt tgtaaattta aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acatatttgt tttctgcacc 240
agaggggaac tgtcaaaata tagagtccca aaccttctgg atctctacca gcaatgtgga 300
attatcacc atcatcatcc aatcgcatg ggagggactc ctgacatagc cagctgctgt 360
gaaataatgg aagagcttac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420

```

240/292

tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tctactata cctgtctgac 480
acaatatcac cagagcaagc catagacagc ctgcgagacc taagaggatc cggggcaata 540
cagaccatca agcaatacaa ttatcttcat gagtttcggg acaaattagc tgcacatcta 600
tcatcaagag attcacaatc aagatctgta tcaagataa 639

<210> 380

<211> 487

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(487)

<223> 5' terminal sequence. max-interacting
protein 1 (MXI1) gene.

<400> 380

aagtggcgac tggaacagct gcagggtcct caggagatgg aacgaatagc aatggacaga 60
attggatcaa ctatttcttc agatcggttct gattcagagc gagaggagat tgaagtggat 120
gttgaaagca cagagttctc ccatggagaa gtggacaata taagtaccac cagcatcagt 180
gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgccca 240
gtgtcaaaact ttcatctact tcatagaacc cagcatgaca taacagtgcg gggaaaatat 300
tcaactgggcc attcatacaa acaatctctt aaattgggtt catgatgcag tctcctcttt 360
aaaacaaaac aaaacaaaac aaactatact tgaacaaaag ggtcagagga ctgttttaag 420
caatacttag caaaagtggg cagctcccaa gagacaattt cagatttcat ttggaaatcc 480
catttta 487

<210> 381

<211> 2416

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2416)

<223> max-interacting protein 1 (MXI1) gene.

<400> 381

agattatgat cgctgaggc ccctctccta cccagatacc gatgttatac tgatgtgttt 60
ttcctttttt tttttttttt tttaagtaat taagggtagt taaattattt aaagtataca 120
aagtccaaac agccaggggt aaggtctcca agaggccttc ccagggttaag ggagtgcgga 180
gaggccccgg tcgccaccgg cggtgcccat ggagcgggtg aagatgatca acgtgcagcg 240
tctgtggag gctgccgagt ttttgagcgg ccgggagcga gagtgtgaac atggctacgc 300
ctcttcattc ccgtccatgc cgagcccccg actgcagcat tcaaagcccc cacggaggtt 360
gagccgggca cagaacacac gcagcgggac gagcaacacc a gcactgccca acagatctac 420
acacaatgag ctggaaaaga atcgacgagc tcatctgcgc ctttgtttag aacgcttaaa 480
agttctgatt ccactaggac cagactgcac ccggcacaca acacttggtt tgctcaacaa 540
agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600
gaatttgga cgagaacaga gatttttaaa gtggcgactg gaacagctgc agggctccta 660
ggagatggaa cgaatacga tggacagcat tggatcaact atttcttcag atcgttctga 720
ttcagagcga gaggagattg aagtggatgt tgaaagcaca gagttctccc atggagaagt 780
ggacaatata agtaccacca gcatcagtga cattgatgac cacagcagcc tgccgagtat 8 40
tgggagtgac gagggttact ccagtgccag tgtcaaactt tcattcactt catagaaccc 900

241/292

```

agcatgacat aacagtgcag ggcaaaatat tcaatgggcc aattcaatac aaacaatctc 960
ttaaattggg ttcattgatc agtctcctct ttaaaacaaa aaaaaacaaa aaaaaactat 1020
acttgaacaa aagggtcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttgtgtg aaattttctt gatttgagtt gattgagaag aggacattgg 1200
agatgccatc ctctttctct tttctcgttt gctcactata cattgagtag acacatttaa 1260
ggatgggggt atgaaccctt cctgagcttt atggctcctaa aagcaaaata aaaactattc 1320
gaatgaaaaa acaagaaaaa caggtattaa tcttgatag ctaataatga gctattaaaa 1380
ctcagcctgg gacagtttat catgaagcct gtggatgata aatcctttat tattattttt 1440
tttttttgaa aaaagctcat ttcattgctt gcaaaaggag agactcccat ga agcctttt 1500
gaaagggatc atcatgcagc tcaactttct gttggattcc atgctaagca agctaaccct 1560
atcctgcatt gttagcacta ggcaccagc tgccacctct ccactctgct gcccttaggc 1620
cacatgggag cagtcctatc atgacagcct ctatcttaca aggcctatga gtatggattg 1680
ggggggccaa aaggaaaaag ctccatg tgc ctctttgtct gcgtgggtca gaagagttgt 1740
gcacgcagat tagcaggcca aggtctgagc cacagcagca tttttatttc agattttgat 1800
aactgtttat atgtgttgaa aacccaaatg acatcttttt aaagcttatc cataaaaaaa 1860
aatagatgac ttttatagtg gaaaaacaca tggggaaaaa aatcatctat ttgatgcag 1920
catttgataa tgataaaaca cctcacacct cactctttat agtgcacaaa atgaatgagg 1980
tctgggctag gtagaaaaag ggtcaatgct atttttgttt ttagaatcat taccttttac 2040
cagcttttaa ccactctgata tctatagtag acacactatc atagttaaca tagttaagtt 2100
cagcacttgt ctcattttaa tgtaaagatt tgcttccatt ttccctacagg cagtctctct 2160
cttcctcaca gtcccactgt gcaggtgcta ttgttactct tacgaatatt ttcagtaatg 2220
ttattttctt ctaagtgaag tttctagcct gcactttgat gtcattgtgt ccctttgtct 2280
ttcaaactcc aaggttcccc tgtggccctc tcccttacc tggaaggcc tcttgagac 2340
cttaccctg gctgt ttgga ctttgtatac tttaaataat ttaactacc ttaattactt 2400
aaaaaaaaaa aaaaaa 2416

```

<210> 382

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(378)

<223> 3' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 382

```

tttttttttt ttgttatagt tacttcaagt aacacagctt gcttcatata aataagttaa 60
aacatctatt ttttttcaag acaaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgc tata atggcaataa acaggctcat gattaaaaga tgaattaggg 180
caacgagaac agggcttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggata cgctaaatac tgctcagtag tttaaacgct cagataactca 300
gggacggaag gccctccctt gcccgcggn atnctccatg gcttttcagc ttattatc tt 360
ttttccactt caatcncc 378

```

<210> 383

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

242/292

<221> misc_feature
<222> (1)..(439)
<223> 5' terminal sequence. homeo box a5 (HOXA5)
gene.

<400> 383
aaatcaagca cacatantan aaaacaaatg agctcttatt ttgtaaactc attttgcggt 60
cgctatccaa atggcccggg ctaccagttg cataattatg gagatcatag ttccgtganc 120
gagcaattca gggactcggc gagcatgcac tccggcagggt acggctacgg ctacaatggc 180
atggatctca gcgtcggcng ctcngctcc ngcactttgg ctccggagag cgcgcccgca 240
gctacgtnc aagccacgc ggcncactcc aagcccagggt acagcnagcc ggccacgtcc 300
acgcaactcn cctcancncg atccgtgcn ctgctcgcgc gtnggcccct tcgccngga 360
ancgacanna ccaanggcgg gaaaaactcc cttaaggca a ctccagcngg cgcctcgggc 420
cgacngccgg aagcaccga 439

<210> 384
<211> 813
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(813)
<223> homeo box a5 (HOXA5) gene.

<400> 384
atgagctctt attttgtaaa ctcatcttgc ggtcgtatc caaatggccc ggactaccag 60
ttgcataatt atggagatca cagttccgtg agcgagcaat tcagggactc ggcgagcatg 120
cactccggca ggtacggcta cggctacaat ggcatggatc tcagcgtcgg ccgctcgggc 180
tccggccact ttggctccgg agagcgcgc cgagctacg ctgccagcgc cagcgcggcg 240
ccgcgcgagc ccaggtacag ccagccggcc acgtccaagc actctoctca gcccgatccg 300
ctgccctgct ccgcctgtgc cccctcgcgc ggcagcgaca cgcaccacgg cgggaaaaac 360
tccctaagca actccagcgg cgcctcggcc gacgccggca gc acccatat cagcagcaga 420
gagggggttg gcaaggcgtc cggagccgag gaggacgccc ctgccagcag cgagcaggcg 480
agtgcgcaga ggcagccgag cccggcgcgc cccgcccaac cccagatcta cccctggatg 540
cgcaagctgc acataagtca tgacaacata ggcggcccg gaggcaaaag ggcccggacg 600
gcctacacgc gctaccagac cctggagctg gagaaggagt tccacttcaa ccgttacctg 660
accgcagaa ggaggattga aatagcacaat gctctttgcc tctccgagag acaaattaaa 720
atctggttcc aaaaccggag aatgaagtgg aaaaaagata ataagctgaa aagcatgagc 780
atggccgcgg caggaggggc cttccgtccc tga 81 3

<210> 385
<211> 447
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(447)
<223> 3' terminal sequence. x-box binding protein
1 (XBP1) gene.

<400> 385

243/292

```
gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca cttttcagaa 60
gctacactag caggaaaaaa ttccatcaag catttacata gtaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaaa gagccccctc agcagggtgtt 180
cccgttgctt acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaatac cttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaatctt aaaagctgta gttctcaatt atagtaatat ttcntacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgtc 447
```

<210> 386

<211> 462

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(462)

<223> 5' terminal sequence. x-box binding protein
1 (XBP1) gene.

<400> 386

```
aagaacctgt agaagatgac ctcggtccgg agctgggtat ctcaaactctg ctttcatcca 60
gccactgccc aaagccatct tcctgcctac tggatgctta cagtgaactgt ggatacgggg 120
gttccctttc cccattcagt gacatgtcct ctctgcttgg tgtaaaccat tcttgggagg 180
acacttttgc caatgaactc tttcccca gc tgattagtgt ctaaggaatg atccaatact 240
gttgcccttt tccttgacta ttacactgcc tggaggatag cagagaagcc tgtctgtact 300
tcattcaaaa agccaaaata gagagtatac agtcctagag aattcctcta tttgttcaga 360
tctcatagat gacccccagg tattgtcttt tgacatccca agcagtccaa ggtattggag 420
acatattact gggaagtaaa gaaatattac tnataattgg ag 462
```

<210> 387

<211> 1836

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1836)

<223> x-box binding protein 1 (XBP1) gene.

<400> 387

```
ggcgctgggc ggctgcggcg cgcggtgcgc ggtgcgtagt ctggagctat ggtggtggtg 60
gcagccgcgc cgaacccggc cgacgggacc cctaaagtgc tgcttctgtc ggggcagccc 120
gcctccgccc cgggagcccc ggccggccag gccctgcgc tcattggtgcc agcccagaga 180
ggggccagcc cggaggcagc gagcgggggg ctgccccagg cgcgcaagcg acagcgcctc 240
acgcacctga gccccgagga gaaggcgtg aggaggaaac tgaaaaacag agtagcagct 300
cagactgcca gagatcgaaa gaaggctcga atgagtgaac tggaacagca agtggttagat 360
ttagaagaag agaaccaaaa acttttgcta gaaaatcagc ttttacgaga gaaaactcat 42 0
ggcctttag tagtagaacca ggagttaaga cagcgcttgg ggatggatgc cctggttgct 480
gaagaggag cggaagccaa ggggaatgaa gtgaggccag tggccgggtc tgctgagtcc 540
gcagcactca gactacgtgc acctctgcag cagggtgcagg ccagttgtc acccctccag 600
aacatctccc catggattct ggcggtattg actcttcaga ttcagagtct gatatcctgt 660
tgggcattct ggacaacttg gaccagtcga tgttcttcaa atgcccttcc ccagagcctg 720
```

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```

ccagcctgga ggagctccca gaggtotacc cagaaggacc cagttcctta ccagcctccc 780
tttctctgtc agtggggacg tcatcagcca agctggaagc cattaatgaa ctaattcgtt 840
ttgaccacat atataccaa g cccctagtct tagagatacc ctctgagaca gagagccaag 900
ctaattgtgt agtgaatac gaggaagcac ctctcagccc ctgagagaat gatcaccctg 960
aattcattgt ctgagtgaag gaagaacctg tagaagatga cctcggttccg gagctgggta 1020
tctcaaatct gctttcatcc agccaactgcc caaagccatc ttctgccta ctggatgctt 1080
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tctaaggaat gatccaatac tgttgccctt ttcttgact attacactgc ctggaggata 1260
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gcagccaag gtattgagac atattactgg aagtaagaaa tattactata attgagaact 1440
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tatgtaaggg tcattagaca aatgtcttga agtagacatg gaatttatga atggttcttt 1560
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gtaagatcaa gaatcttttg tgaattata gaaatttact atgtaaat gc ttgatggaat 1740
tttttctgc tagtgtagct tctgaaagg gctttctcca tttattttaa actaccatg 1800
caattaaaag gtacaatgca aaaaaaaaa aaaaaa 1836

```

<210> 388

<211> 433

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 388

```

tttttcttaa ataatttatt ttttaatgtt gactcttggtg aaaagttaca tttattttaga 60
aaaacttgaa gaaatccaac aaagaatagg tggctttcta ttaggggacaa ttaaatgtgc 120
aaatttcaaa tactttttat aataagtata aataattact ttttttcaca ttaagaatgg 180
aaataatgat caacacaana tattaagata tcaactttta gagaattaga tgaaaacact 240
gaagtttatt tngtatctt tgaaaangaa ttataaagat tcgtctggga aaaactt agg 300
gggctctaag gggaaagttg tgcctaatag tatgagtaaa ggctgtgtag agttatggat 360
cacaaatatt ttcaggcctt aagtacagac ccccnaaatg gcagccttta tcncggggga 420
aatgcattt ccc 433

```

<210> 389

<211> 206

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,
alpha-induced protein 3 (TNFAIP3) gene.

<400> 389

245/292

```
ctcaaccagc tgccttttta aaggga gctc tagtcctttt tgtgtaattc actttattta 60
ttttattaca aacttcaaga ttatttaagt gaagatattt cttcagctct ggggaaaatg 120
ccacagtgtt ctctgagag aacatccttg ctttgagtca ggctgtgggc aagttcctga 180
ccacagggag taaatngnn cctctt 206
```

<210> 390

<211> 4426

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(4426)

<223> tumor necrosis factor, alpha -induced protein
3 (TNFAIP3) gene.

<400> 390

```
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agcacaatgg ctgaacaagt ccttctcag gctttgtatt tgagcaatat gcggaaagct 120
gtgaagatac gggagagaac tcagaagac atttttaaac ctactaatgg gatcattcat 180
cattttaaaa ccattgcaccg atacacactg gaaatgttca gaacttgcca gtt ttgtcct 240
cagtttcggg agatcatcca caaagccctc atcgacagaa acatccaggc caccctggaa 300
agccagaaga aactcaactg gtgtcgagaa gtccggaagc ttgtggcgct gaaaacgaac 360
ggtgacggca attgctcat gcatgccact tctcagtaca tgtggggcgt tcaggacaca 420
gacttggtac tgaggaaggc gctgttcagc a cgctcaagg aaacagacac acgcaacttt 480
aaattccgct ggcaactgga gtctctcaaa tctcaggaa ttgttgaaac ggggctttgc 540
tatgatactc ggaactggaa tgatgaatgg gacaatctta tcaaaatggc ttccacagac 600
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ctttgaaca tcctcagaag gccaatcatt gtcatctcag acaaaatgct aagaagtgtg 720
gaatcagggt ccaatttcgc ccttttgaaa gtgggtggaa tttacttgcc tctccactgg 780
cctgcccagg aatgctacag atacccatt gttctcggct atgacagcca tcattttgta 840
cccttggtga ccctgaagga cagtgggcct gaaatccgag ctgttccact t gttacaga 900
gaccggggaa gatttgaaga cttaaaagtt cactttttga cagatcctga aaatgagatg 960
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ccaaccaga ggatgggccc tggggccac cggggtgagc ctgccccga agaccccc 2340
aagcagcgtt gccgggcccc cgctgtgat cttttggca atgccaagt caacggctac 2400
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```

tgcaacgaat gctttcagtt caagcagatg tatggctaac cggaaacagg tgggtcacct 2460
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gctgccactg caacagtggg ctttaggggtg tctgagcagg agaggaaaga taagctcttc 2580
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taaattgtaac ttttcacaag agtcaacatt aaaaaataaa ttattt 4426

```

<210> 391

<211> 440

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(440)

<223> 3' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 391

```

ttttttgtg cacaaaaatg atacatttat tgaaagagta tttttttttt aatacaaaag 60
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agtagaaacc actgacatac acactcacat tcaagcacac acactcactc aggcgcacac 180
acccacacac acatacccca gagccaccga ggaagggaac caccaagggt cgctgcacat 240
aaaaatatca cctcaactca tccctgacac agcgtgtcc tcccaaggcc acgctcacac 300
aacacacatt ataagcactt tgcctgattc actcactngg gtctgtcttt tgtgggaagg 360
agagggaaga ttcatcaaag gtctcctccc catgggtngg gggagtgggg agtgagttag 420
tgatggtgga gtgaaacaag

```

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<210> 392
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(471)
<223> 5' terminal sequence. serum response factor
(c-fos serum response element-binding
transcription factor) (SRF) gene.

<400> 392
aattcggcac gaaggcagga atgggggtca gaagaagtgg gagcagcttc ttgggctgag 60
tcgagcaaaag gggagccaga aatgggcagt tctcccaggg agtgagcagc tactgtaact 120
tttttaaat aagacaaaaa gccttgaaga aaatgacttt atttttctaa gtgtaacctc 180
agtatttatg taatttgtac aggggccatg ccacncccc tctccccct ttngtnaga 240
ccttgagggt gggccagcat aggggggagg gtcttttacc ctgtgtcaga gcctaccttc 300
accacctata tcagaaggg gagctttttc agaaacaggg cagcagtggg gtgaaatatt 360
cttaaccct aagactgcct tcagtaagga acaagctggc ttctgtgatt aggtgaaggg 420
atgggggaag attttaatgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393
<211> 4201
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(4201)
<223> serum response factor (c-fos serum response
element-binding transcription factor) (SRF) gene.

<400> 393
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ccgcgccag cagcccctgc cccccgggg acgctgacgg ccgcccggcg cgccgcccta 120
gcagacggac agggggcgct gcgcgcggcc tggggcaacc cgggccac ag gggcaggaaa 180
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tgaagagaca gatctcacct accaggtgtc ggagtctgac agcagtgggg agaccaagga 1140

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cacactgaag ccggcggttca cagtacacaa cctgccgggt acaacctcca ccatccaaac 1200
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agaaacaggg cagcagtggt gtgaaatttt cttaaccct aagactgcct tcagtaggaa 3480
caagctggct tctgtgatta ggtgaaggga tgggggaaga ttttatgcac agcctagtta 3540
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ttctacttcc cctgggatgc tgaccagga atagtggaca tggtcacagt cctatgtaca 4140
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g 4201

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<210> 394

<211> 563

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(563)
<223> 3' terminal sequence. sry (sex determining
region y)-box 9 (campomelic dysplasia, autosomal
sex-reversal) (SOX9) gene.

<400> 394
tttttaaatgc aatgtatatatt tattgtaaac aataatatac aaaaaaaaaa aagagaaaga 60
aaaagggaaa ggtaagtttc acggagagaa caaaagggttt ggggctggga gggaaacaag 120
tgaacaaac aaaacacgaa cacaaccaa agcttttacc taaagacaaa atatgattta 180
aatgccagggt ttcttaagtt acaga agtat ctttttaaaa agatctgctt ttatacagaa 240
attgaaggat gccatattat gagtgtttta agattttatt ctactgactt ctaaaactgt 300
taatatatct ttttttaaat aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatcctc 360
aaactctcta gccacagcag taattaagat taagggtctgt cagtgggctg atcccctcca 420
ggtagcctcc ctactccaa gagaagatgc ngagaaatat gggatggaca catgcctgca 480
tgtttttgtg nccaaacaca cacanacca nacacacnca caatataagg cngccccaag 540
gtctntggcc gaaancctgg caa 563

<210> 395
<211> 3936
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3936)
<223> sry (sex determining region y) -box 9
(campomelic dysplasia, autosomal sex -reversal)
(SOX9) gene.

<400> 395
ggagagccga aagcggagct cgaaactgac tggaaacttc agtggcgcgagg agactcgcca 60
gtttcaacc cggaactttt tctttgcagg aggagaagag aaggggtgca agcgcccca 120
cttttgctct ttttctctcc ctctctctcc tctocaattc gcttcccccc acttgagcgg 180
ggcagctgtg aactggccac ccgcgcctt cctaagtgtc cgccgcggta gccggc cgac 240
gcgccagctt ccccgaggag cgcttgctcc gcatccgggc agccgagggg agaggagccc 300
gcgcctcgag tcccagagcc gccgcggctt ctgcctttc ccggccacca gcccctgcc 360
ccgggcccgc gtatgaatct cctggacccc ttcatgaaga tgaccgacga gcaggagaag 420
ggcctgtccg gcgccccag cccaccatg tccg aggact ccgcgggctc gccctgcccg 480
tcgggctccg gctcggacac cgagaacacg cggccccagg agaacacgtt cccaagggc 540
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ggctccagca agaacaagcc gcacgtcaag cggcccatga acgccttcat ggtgtgggag 720
caggcggcgc gcagggaagct cgcggaccag taccgcact tgcacaacgc cgagctcagc 780
aagacgctgg gcaagctctg gagacttctg aacgagagcg agaagcggcc ctctgtggag 840
gaggcgaggc ggctgcgcgt gcagcacaag aaggaccacc cggattacaa gtac cagccg 900
cggcgaggag atcggttgaa gaacgggcag gcggaggcag aggaggccac ggagcagacg 960
cacatctccc ccaagcccat ctcaaggcg ctgcaggccg actcgccaca ctctcctcc 1020
ggcatgagcg aggtgcactc ccccggcgag cactcggggc aatcccaggg cccaccgacc 1080
ccaccacca ccccaaaaac cgacgtgcag ccgggcaagg ctgacctgaa gcgagagggg 1140
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gagctgagca gcgacgtcat ctccaacatc gagaccttcg atgtcaacga gtttgaccag 1260
tacctgccgc ccaacggcca cccgggggtg ccggccacgc acggccaggc cacctacacg 1320
ggcagctacg gcatcagcag caccgcgcc acccgcgga gcgcgggcca cgtgtggatg 1380
tccaagcagc aggcgcgcgc gccacccccc cagcagcccc cacaggcccc gccggccccg 1440

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caggcgcccc cgcagccgca ggcggcgccc ccacagcagc cggcgggcacc cccgcagcag 1500
ccacagggcg acacgctgac cagcgtgagc agcagagccgg gcca gtccca gcgaacgcac 1560
atcaagacgg agcagctgag cccagccac tacagcgagc agcagcagca ctgccccaa 1620
cagatcgct acagcccctt caacctccca cactacagcc cctcctacc gcccatcacc 1680
cgctcacagt acgactacac cgaccaccag aactccagct cctactacag ccacgcggca 1740
ggccagggca cgggctct a ctccacctt acctacatga acccgctca gcgccccatg 1800
tacaccccca tcgcccagac ctctggggtc ccttccatcc cgcagacca cagccccag 1860
cactgggaac aaccgctota cacacagctc actcgacctt gaggaggcct cccacgaagg 1920
gcgagatgg ccgagatgat cctaaaaata accgaagaaa gagaggacca accagaat tc 1980
cctttggaca tttgtgtttt tttgtttttt tttttgttt tgttttttct ttttcttctt 2040
cttcttaaa gacatttaag ctaaaggcaa ctgtagcca aatttccaag acacaaacat 2100
gacctatcca agcgatttac ccacttgttg ccaatcagtg gccaggccaa ccttggctaa 2160
atggagcagc gaaatcaacg agaaactgga ct ttttaaac cctcttcaga gcaagcgttg 2220
aggatgatgg agaatcggtg gatcagtggt ctaaattctt ctgcctgttt ggactttgta 2280
attatttttt tagcagtaat taaagaaaaa agtctctgtt gaggaatatt ctctatttta 2340
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tttagataaa attaaatgct cttatttttc caacagctaa actactctta gttgaacagt 2460
gtgccctagc ttttcttgca accagagtat tttgtacag atttgcttcc tcttacaaaa 2520
agaaaaaaa aatcctgttg tattaacatt taaaaacaga attgtgttat gtgatcagtt 2580
ttgggggtta actttgctta attcctcagg ctttgcgatt taagga ggag ctgccttaaa 2640
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gtaagcttta tgatatatat attttttaa gaagagaaaa acaccttgag ccttaaaaacg 2760
gtgctgctgg gaaacatttg cactctttta gtgcatttcc tcctgccttt gcttgttcac 2820
tgcagtctta agaaagaggt aaaaggcaag caaaggagat gaaatctgtt ctgggaatgt 2880
ttcagcagcc aataagtgcc cgagcacact gccccgggtt gcctgcctgg gcccatgtg 2940
gaaggcagat gcctgctcgc tctgtcacct gtgcctctca gaacaccagc agttaacctt 3000
caagacatcc cacttgctaa aattatttat tttgtaagga gaggttttaa ttaaaacaaa 3060
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cttaaaagcac tcataatatg gcaccttca attctgtat aaaagcag at ctttttaaaa 3720
aagatacttc tgtaacttaa gaaacctggc atttaaatca tttttgtct ttaggtaaaa 3780
gctttgggtt gtgttcgtgt tttgtttgtt tcaattgttt ccctcccagc cccaaacctt 3840
ttgttctctc cgtgaaactt accttccct ttttcttct cttttttttt ttgtatatta 3900
ttgtttacaa taaatataca tt gcattaaa aagaaa 3936

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<210> 396

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(204)

<223> 3' terminal sequence. cadherin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 396

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tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggaggt 60
tgctgtcttt canacaaaga tgaggttcac tgnnaggagg caaagggtggg actaggaggag 120

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tgacccgcat gggccagatn ggagagaaac tcttcccacc ccggcagaag gggcctcttc 180
ctggccgccc catccanact cagg 204

<210> 397

<211> 458

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(458)

<223> 5' terminal sequence. cadhe rin 15,
m-cadherin (myotubule) (CDH15) gene.

<400> 397

caggacgcct acgacatcag ccagctgcgt caccgcagag cgctgagcct gcctctggga 60
ccgcgcgccac ttcgcagaga tgcccgcag ncagcctgca ccccagcca ccccgagtgc 120
tgcccaccag cccctggac atcgccgact tcatcaatga tggcttga g gctgcagata 180
gtgacccag tgtgcgcct tacgacacag ccctcatcta tgactacgag ggtgacggct 240
cggtggcggg gacntgagct ccctcctgtc cagccagggc gatgaggacc aggactacga 300
ctacctcaga gactgggggc cccgcttcgc ccggctggca gacatgtatg ggcacccgtg 360
cgggttngga gttacggggc cagatgg gac caccaggcca gggagggctt ttctcctggg 420
gcactgctac ccagacacag aggcgggaca gcctgan 458

<210> 398

<211> 2833

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2833)

<223> cadherin 15, m-cadherin (myotubule) (CDH15)
gene.

<400> 398

acttgcgctg tactcagcc tggacgcgt tcttcgggtc gggggtgcac tccggcccg 60
ctcccgcctc ggcccgatg gacgcgcgt tctcctcgt cctcgggctg ttggcccaga 120
gcctctgcct gtctttggg gtt cctggat ggaggaggcc caccacctg taccctggc 180
gccgggcgcc tgccctgagc cgcgtgcgga gggcctgggt catcccccg atcagcgtat 240
ccgagaacca caagcgtctc ccctacccc tgggtcagat caagtcggac aagcagcagc 300
tgggcagcgt catctacagc atccaggac ccggcgtgga tgaggagccc cggggcgtct 360
tctctatcga caagttcaca ggaaggtct tctcaatgc catgctggac cgcgagaaga 420
ctgatcgtt caggctaaga gcgtttgcc tggacctggg aggatccacc ctggaggacc 480
ccacggacct ggagattgta gttgtggatc agaatgacaa ccggccagcc ttcctgcagg 540
aggcgttcac tggccgcgtg ctggagggtg cagtcccagg cac ctatgtg accagggcag 600
aggccacaga tgccgacag cccgagacg acaacgcagc gctgcggtc tccatcctgc 660
agcagggcag ccccgagctc ttcagcatc agagctcac aggagagatc cgcacagtgc 720
aagtggggct ggaccgcgag gtggtgcggt tgtacaatct gaccctgcag gtggcggaca 780
tgtctggaga cggcctcaca g cactgcct cagccatcat caccctgat gacatcaatg 840
acaatgcccc cgagttcacc agggatgagt tcttcatgga ggccatagag gccgtcagcg 900
gagtggatgt ggacgcctg gaagtggagg acaggacct gccaggctcc ccaaactggg 960
tggccaggtt caccatcctg gaaggcgacc ccgatgggca gttcaccatc cgcacggacc 102 0

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ccaagaccaa cgagggtgtt ctgtccattg tgaaggccct ggactatgag agctgtgaac 1080
actacgaact caaagtgtcg gtgcagaatg agggcccgct gcaggcggct gcccttaggg 1140
ctgagcgggg ccaggccaag gtccgcgtgc atgtgcagga caccaacgag ccccccgtgt 1200
tccaggagaa cccacttcgg accagcctag cagagggg gc acccccaggg actctggtgg 1260
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ggcgagggcc caagtctggg ggcagaacct gagtgtggat ggggcggcca ggaagaggcc 2700
ccttctctgc ggggtgggaa gagtttctct ccacggccc catgcgggtc acc tccctag 2760
tccaccttt gcctctacc agtgaacctc atctttgtat gaaagacagc aacctcctgg 2820
gtaaatctga atg 2833

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<210> 399

<211> 646

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> misc_feature

<222> (1)..(646)

<223> 3' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 399

```

tatctcacac tgtactttat tttcttcac aatattaact agacagacaa ggaaagtta 60
atggcaatgt gactttttcc aacaacacaa acaaagtgcc attata gcta atggtggcca 120
actggagact tactttacct taacctatga aagtatcctt accgtatttt ttatgtgtac 180
agtgttgtag aatatcagcc acctcttaaa agtatcaatc ttaaaaagag ccatggaagg 240
taaaagtatg aaaatcttga taacaaaagc tttaataca aaaacactta ttgtacactt 300
atttttattt aaacaaaaaa taac ccagat aactcaaaac aaaagcaaac cttggttgaa 360
aacttaagaa ggtataataa acaaaaccac caaaagaaag cttcccaaaa agaaatgcaa 420
tccactgtca ctcttgcaaa ttctaccttg gagggaaaaa cttaatgaaa tgagctatct 480
ggaggggccc cggagatttt caaaagggtt taggtgcatg gatttactca gtatctacnt 540
acagtcttat ttattaatag ctcaganttc ctgattgagc gagcctttcc atctccacca 600
gtgtcccccac ttctgtgcnc acttgggntg cagacaccct gtgttg 646

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<210> 400
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(465)
<223> 5' terminal sequence. b-cell cll/lymphoma 2
(BCL2) gene.

<400> 400
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ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaa aattttataa 1 20
aattaagcaa tgtgaaactg aattggagag tgataataca agtccttttag tcttaccag 180
tgaatcattc tgttccatgt ctttggacaa ccatgacctt ggacaatcat gaaatatgca 240
tctcactgga tgcaaagaaa atcagatgga gcatgaatgg tactgtaccg gttcatctgg 300
actgccccag aaaaaataact tcaagcaaac atcctatcaa caacaagggtt gttctgcata 360
ccaagctgag cacagaagat gggaacactg gtggaggatg gaaaggctcg ctcaatcaag 420
aaaattctga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(419)
<223> 3' terminal sequence. ests (EST W73386)
gene.

<400> 401
gaaggtcatt cttgcgatgg gtttattgca ggagatgatg gaccaaagg ctctgacaca 60
tgcacacgct cctgggcacg cctgctgcgn gtncgcttcc catga cccc agggccctct 120
atgcctccc cccagggcac cctgccact tgccccact tcatgtacca ccaagccctt 180
tccttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagt catgtggctc 240
agaacataaa agcatcttca acattcgtca ttgagccaaa cgaaacacag tgtttggtc 300
aagagccggc gacactngca tcc ctatcca cacgtggaac ctgcccttgg gcttngttga 360
ccggaggatn ggccgctctt ccttgtcatc cagcancgg agcatgtatg tgcccaga 419

<210> 402
<211> 568
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(568)
<223> 3' terminal sequence. granzyme a (granzyme

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1, cytotoxic t-lymphocyte-associated serine
esterase 3) (GZMA) gene.

<400> 402

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tcatgcaaat tgattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaaacg 60
gttattttaa ctgctccctt gatagt cata attatccagt tgagggtgtt ctttgagaga 120
agaatataga caccaggccc acgagggtct ccgcatttat tttcaaggcc aaaggaagtg 180
accctctgga aaacaccctc gcacaacaaa gggcttccag aatctccatt gcacgagtct 240
cttccacctc ggaggcttcc agcacaaccc atattcattc caatcacagg gttaaaatta 300
tagtgatttc gatcattgca gacttttctg tctatgatgg gtgatattga cttgactca 360
gagtatcggg acccaagatg cactattggg gagtcctgcc ccaccctggc aacttggcac 420
atggttctctg gntttcacat caatccccct ttttagggag atgaaggata gtcacatatn 480
tggtnathtt ggctttttcc ggtcagctgt aaagttttta ggtccc ctnc gcgtttggtg 540
gggcctagcc tgggnaggga aanccttt 568
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<210> 403

<211> 878

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(878)

<223> granzyme a (granzyme 1, cytotoxic
t-lymphocyte-associated serine esterase 3) (GZMA)
gene.

<400> 403

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cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcctc tctctcagtt gtcgtttctc tcctgctaatt tcctgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactcctc attcaagacc ctacatggtc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgcttggtta agaaagagtt tcc ctatcca tgctatgacc 360
cagccacacg cgaagggtgac cttaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaaaa agggggatga tgtgaaacca ggaaccatgt 480
gccaagttgc aggtgggggg aggaactaca atagtgcac ttgggtccgat actctgagag 540
aagtcfaatc caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
accctgtgat tggaaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctggaagc cctttgttgt gcgagggtgt tttccgaggg gtcacttctc 720
ttggccttga aaataaatgc ggagaccctc gtgggcctgg tgtctatatt cttctctcaa 780
agaaacacct caactggata attatgacta tcaagggagc agtttaaata accgtttcct 840
ttcattttact gtggcttctt aatcttttca caaataaa 878
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<210> 404

<211> 191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(191)

<223> 3' terminal sequence. v-fos fbj murine

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osteosarcoma viral oncogene homolog (FOS) gene.

<400> 404

```
gcagtgaccg tgctcctacc cagctctgct tcacagcgcc cacctgtctc cgcccctcgg 60
ccccctgccc ggctttgcta accgccacga t gatgttctc gggtttcaac gcagactacg 120
aggcgtcatc ctcccgctgc agcagcgct ccccgccgg gataanctct ctttattaca 180
attaatcanc g 191
```

<210> 405

<211> 245

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(245)

<223> 5' terminal sequence. v-fos fbj murine
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 405

```
ttttcaactt aaatgctttt attgacaatg tcttgaaca ataagcaaac aatgcttaaa 60
tttttcattc aaattcactt tccacatgtc aaaagacctc aaggtagaaa aaaataaaat 120
aaaaatataa atatctgaga atccatctta ataaataaat taaaaacaca ataaaacgtt 180
tcatggaaa actgttaatg tccngaacat tcagaccacc tcnacaatgn gtgntongtn 240
anatt 245
```

<210> 406

<211> 489

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(489)

<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 406

```
gcgncgcgct caccgaagg ngnangtaga cagcgggtca gaggccgcct agagccggag 60
gacaccccaa atacaaacat accacggaga gacctgggat ctgagtttca aaagggcctg 120
tgataaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaatactt aggagacttg tt ttactcag agtggaat tttgccaggg acaaagtcaa 240
cacaagaaaa caaacaacaa aaaatagcca gaaagagaac agttaagtgc agtcgggtga 300
gtcccggcag ttccctcccg gcaactggctc gtccctgggt tctcaagggt ccatgcggcc 360
acagcgctcg tccacctgtc cagcggagcc acatgtctgaa atgggaggtg ggataaaatt 420
catcaggcag ctgctgtaac acggaaatgt gcagatgcca gagtagcttc gtctgaactt 480
gaacaagac 489
```

<210> 407

<211> 247

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(247)
<223> 5' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 407
tggtttcagc ctatggaatg atttcctttt gtctgtcttg ttcaagttca gacgaagcta 60
ctctggcacc tgcacatttc cgtgttacag cagctgcctg atgaa ttta tccacctcca 120
tttcagcatg tggctcgcgt ggacaggtgg acggacgctg tggccgcatg gaaccttgag 180
aaccaggga cgagccagtg ccgggaagga actgccggga ctaccganc tgcncttaac 240
tggtctc 247

<210> 408
<211> 3059
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(3059)
<223> interleukin enhancer binding factor 1 (ILF1)
gene.

<400> 408
gccccccccc cagcctcct cccctcctcc cgcccgcgcg tgctcccgcc cctcgccgcc 60
gtctgctcgc tcgcccggcg gcctccgctc ggccccctcc ctacagctccg gtgcgcggcg 120
gccgacgacc cgcggccttg gcctcggcgc gccaccggcg ccgcgcggga gcggcccggg 180
ggccctcaag caggcccatg gcggcggcgc gcgcgctct cgggcggggc accacgcggg 240
cgcgggggcg ggggcgcggg gcccggggcg ggtcccgccg ggcgctgggc cgtggggcgc 300
ctggaggggc gcgagtcca gtatctgat aagaagcgct cggtgacct cggccgcaac 360
tcgtcgcagg gctcgggtga cgtgagcat ggccactcga gcttcattct ccggcgccac 420
ctcgagatct tcacgcccc gggcggcgcg gccatggcgg ggccgctccg gagctgccgc 480
ccgcgcagcc caggcccgac gccggcggcg acttctacct gcgctgcttg ggcaagaacg 540
gggtattcgt ggacggcgtg ttccagaggc gcggggcgcc gccgctgcag ctgccgcgcg 600
tgtgcacatt caggttcccg agcacaaca tcaagataac gttcactgcc ctgtccagcg 660
agaagagaga gaagcaggag gcgtctgagt ctccagtga a ggccgtacag ccacacatct 720
cgccctgac catcaacatt ccagacacca tggcccacct catcagccct ctgccctccc 780
ccacgggaac catcagcgct gcaaaactcct gccctccag ccccgggga gcgggggtctt 840
cagggtacaa ggtgggccga gtgatgccat ctgacctcaa tttaatggct gacaactcac 900
agcctgaaaa tgaaaag gaa gcttcagggt gagacagccc gaaggatgat tcaaagccgc 960
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ccctgaacgg gatttataca cacatcacta aaaattatcc ctactacagg actgcggaca 1080
agggctggca gaattcaatt cgcacaatc tctctctgaa tcgttatttc atcaaag tgc 1140
cgcggtccca ggaagaacca ggcaaaggct cgttctggag gatagacca gcctctgaaa 1200
gcaaattaat agaacaggct tttaggaaac gcggcctag gggcggtgcc tgcttttagaa 1260
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agcggcagct accacaggcc atcaagcctg tcacctacac tgtggccacc ccagtgacca 1560
cctcgacctc ccagccaccc gtcgtgcaga cgttcacgt cgctccaccg atcccagcgg 1620
tgtcggtcac cagtgtggcc ggactggccc cagcgaacac gtacactgtc tctggacaag 1680

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```
ctgtggtcac cccggcagcc gtgctggccc ctctaaggc agaggcccag gagaatggag 1740
accacagga agtcaaagt aaagtagagc ctattcccgc cattg gccac gccacgctcg 1800
gcaactgcc cccgatcatt cagacggcac agaccacccc ggtccagacg gtgaccatag 1860
tacaacagga acctctaggt caacaccagc taccaataaa aactgtaaca caaacggca 1920
ctcacgtggc atcagtcacc actgcggtcc acggccaggt gaacaatgcc gcggcgagtc 1980
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tcgtcattgc cctgagcgtg gacacgccac cggcagccgt aagggaaaag ggtgtccaga 2160
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cggcctcccg ccagcactcg ggggtgcagg gccctgtggt tggacttcac ctctcagcac 2280
tgaaaaccca aaacccagct ggccttaaca ctccctaaag acagaagtca cacttgaaca 2340
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tgtgttgact ttgtccctg caaaattttc cactctgagt aaaacaagtc tcggaattc 3059
```

<210> 409

<211> 201

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(201)

<223> 3' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDIA) gene.

<400> 409

```
tttttttttt tccttcaggg gcatttattt cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gcttggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggctct cagcaatgtg tgcacttggt cccttgtttg ttcttggtg ggtcagggaa 180
ggcctgccgn ggggtggtggc a 201
```

<210> 410

<211> 297

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(297)

<223> 5' terminal sequence. rho gdp dissociation
inhibitor (gdi) alpha (ARHGDIA) gene.

<400> 410

258/292

ggcctctgct gccctttctg tgccccccag gttctatctc cccgtcacac ccgaggcctg 60
gcttcaggag ggagcggana gccattctcc agggcccggtg gttgcccctg gacgtgtgcg 120
tctgctgctc cggggtggan ctggggtgtg ggatgcacgg cctcgtgggg gccgggcccgt 180
cctccagccc cgtgctccc tggccagccc cc ttgtcgtc gtcgggtccc tctaaccatg 240
atgccttaac atgtggagtg tacctgtggg gcctcactaa gcctctaant cactgtg 297

<210> 411

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> rho gdp dissociation inhibitor (gdi) alpha
(ARHGDI A) gene.

<400> 411

cctgaaccgc gcggccgaac cctccgggtgt cccgaccag gctaagcttg agcatggctg 60
agcaggagcc cacagccgag cagctggccc agattgcagc ggagaacgag gaggatgagc 120
actcgtcaa ctacaagccc ccggcccaga agagcatcca ggagatccag gagctggaca 180
aggacgacga gagcctgcga aagtacaagg aggcctgct gggccgcgtg gccgtttccg 240
cagacccaa cgtcccacac gtctgtgtga ctggcctgac cctggtgtgc agctcggccc 300
cgggcccctt ggagctggac ctgacggggc acctggagag cttaagaag cagtcgtttg 36 0
tgctgaagga ggggtgtggag taccggataa aaatctcttt ccgggttaac cgagagatag 420
tgtccggcat gaagtacatc cagcatatgt acaggaaagg cgtcaagatt gacaagactg 480
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aggaggcacc caaggggtatg ctggcccggg gcagctacag catcaagtcc cgcttcacag 600
acgacgaaa gaccgaccac ctgtcctggg agtggaatct caccatcaag aaggactgga 660
aggactgagc ccagccagag gcgggcaggg cagagtgtat gacggaagac ggacaggcgg 720
atgtgtcccc cccagcccct cccctcccca tacciaagggt ctgagcaggc cctccgtgcc 780
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accaagtgca cacattgctg agagccgtct cctataggct ccccgcccca tccccgtgt 1740
tggtgtgtg tctgccaggc tcaggcagag gcgcctgtcc ctgcttcttt tctgaccggg 1800
aaataaatgc ccctgaagg 1819

<210> 412

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(306)

<223> 3' terminal sequence. complement component
4a (C4A) gene.

<400> 412

```
gctgccaaaa gcctttaata tgccctggtc ccaggctgt g ttcattgaaag cggacacagc 60
agtgttcca gcttcatggt tcccagggtc aggttcctcc cagcggaggt gggagggcag 120
ccctcacacc tggcaccctt gattgcatac tcttgaggga agtcgttgag ctgggcacag 180
gctgcccgct ggcggttgcn tccggcacag gcgttcagag ggcatctcct cgatccagct 240
attcgagtcc agcaagta ct ngggggggnc cctcccaggg gcataantng gncntccag 300
anccat 306
```

<210> 413

<211> 5417

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(5417)

<223> complement component 4a (C4A) gene.

<400> 413

```
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ctctgggggc tgatctgggc atccagcttc ttcaccttat ctctgcagaa gccaggttg 120
ctcttggttct ctccttctgt ggttcatctg ggg gtcccc tatcgggtggg ggtgcagctc 180
caggatgtgc cccgaggaca ggtagtgaag ggatcagtggt tctgagaaa cccatctcgt 240
aataatgtcc cctgctcccc aaagggtggac ttcaccctta gctcagaaag agacttcgca 300
ctcctcagtc tccagggtgcc cttgaaagat gcgaagagct gtggcctcca tcaactcctc 360
agaggccctg aggtccagct ggtggcccat tcgccatggc taaaggactc tctgtccaga 420
acgacaaaca tccagggtat caacctgctc ttctcctctc gccgggggca cctctttttg 480
cagacgggacc agcccattta caacctgggc cagcgggttc ggtaccgggt ctttgctctg 540
gatcagaaga tgcgcccag cactgacacc atcacagtca tgggtggagaa ctc tcacggc 600
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gaatccaaca gcagcaccga gtttgaggtg aagaaatatg tccttcccaa ctttgaggtg 780
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cattactact acatgacct atcccagggg cagatcgtgt tcatgaatcg agagcccaag 1620
aggacctga cctcgtctc ggtgtttgtg gaccatcacc tggcaccctc cttctacttt 1 680
gtggccttct actaccatgg agaccacca gtggccaact ccctgcaggt ggatgtccag 1740
gctggggcct gcgaggggcaa gctggagctc agcgtggacg gtgccaagca gtaccggaac 1800
```

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```

ggggagtccg tgaagctcca ottagaaacc gactccctag ccctggtggc gctgggagcc 1860
ttggacacag ctctgtatgc tgcaggcagc aagtcc caca agcccctcaa catgggcaag 1920
gtctttgaag ctatgaacag ctatgacctc ggctgtggtc ctgggggtgg ggacagtgcc 1980
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cagcagccgg actgccggga gcccttctcg tcctgctgcc aatttgetga gagtctgcgc 2280
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<210> 414
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(408)
<223> 3' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 414
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gcttttgattc tgggaactga ataggaggag aacacctgga ctactctgag tcctgagttc 240
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<210> 415
<211> 457
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(457)
<223> 5' terminal sequence. cd3g antigen, gamma
polypeptide (tit3 complex) (CD3G) gene.

<400> 415
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tcagacaagc agactctggt gcccaatgac cagctctacc agcccctcaa ggatccgagg 420
aagatgacca gtacagccac cttcaagggn aaccagt 457

<210> 416
<211> 822
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

262/292

<222> (1)..(822)

<223> cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

<400> 416

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<210> 417

<211> 439

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(439)

<223> 3' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b
(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 417

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gccgccccca aaggccgct 43 9
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<210> 418

<211> 234

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(234)

<223> 5' terminal sequence. v-rel avian
reticuloendotheliosis viral oncogene homolog b

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(nuclear factor of kappa light polypeptide gene
enhancer in b-cells 3) (RELB) gene.

<400> 418

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<210> 419

<211> 2314

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2314)

<223> v-rel avian reticuloendotheliosis viral
oncogene homolog b (nuclear factor of kappa light
polypeptide gene enhancer in b -cells 3) (RELB)
gene.

<400> 419

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<210> 420

<211> 214

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 420

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<210> 421

<211> 520

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1
(ESR1) gene.

<400> 421

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<210> 422

<211> 6450

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(6450)
<223> estrogen receptor 1 (ESR1) gene.

<400> 422

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266/292

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gatgtgactc ggttttgtcg cagctttgct ttgtttaatg aaacacactt gtaaacctct 6360
tttgcacttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaacaa ttttctcaac 6420
ctatttgatg ttcaataaaa gaattaaact 6450

```

<210> 423

<211> 580

<212> DNA

<213> Artificial Sequence

267/292

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(580)

<223> 3' terminal sequence. pre -b-cell leukemia transcription factor 1 (PBX1) gene.

<400> 423

```
ttaaacgtac aaacactttt attattttct ttgtaatttt tttcctcttt aaattcctct 60
aattgttgaa aatatccttc agtgatatgc gagagggcgg gcacccggga gtctaggaca 120
gaggcacagg ggcaggggaag atgacgaaaa ccaggctgac agctggaggc agggaagggt 180
ggcttctacc cagaaaaaaa aggggagaga gtataaagaa gtgtccagat tggctgaaat 240
agcatcccaa agaagagaag agaaggagac tottattgtg tttgc tgatt gcttcgacct 300
ccagtctgac cgcttcaggn ttgggagaga aaccctccct tcctgcccct gcccactg 360
ggcgacaggg tcagccggga tgcgattgct gggagatcag ttggaggtat cagagtgaac 420
actgccaggg ccttctgtag gggaggtcac tgatgaaggg gtagtagcat cctgcccaacc 480
tccattagca ctgatgccct gcg gactgta catctgactg gctgcgagtc catcactgta 540
tcctcctgtc tggctgataa catggcgaag ggtatccacc 580
```

<210> 424

<211> 503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(503)

<223> 5' terminal sequence. pre -b-cell leukemia transcription factor 1 (PBX1) gene.

<400> 424

```
gccaaagagg agttagccaa gaagtgtggc accacagtct cccaggtatc acaactggtt 60
tggaaataag cgaatccggt acaagaagaa cataggtaaa tttcaagagg aagccaatat 120
ttatgtctgc aaaacagctg tctactgtac caatgtgtca gcccatggaa gccaaagctaa 180
ctcgccctca actcccaact cggctggttg atacccttcg ccatgttatc agccagacag 240
gaggatacag tgatggactc gcagccagtc agatgtacag tccgcaggca tcagtgtctaa 300
tggagggttg caggatgcta ctacccttc atcagtgacc t cccctacag aaggccctgg 360
cagtgttcac tctgatacct ccaactgata tcccagcaat cgcaccccg ctgaccctgt 420
gccccagttg ggcaggggca ggaggaggg tttctctccc aacgctgaag cggtcagact 480
ggagggtcaaa cgattaggca aac 503
```

<210> 425

<211> 1819

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1819)

<223> pre-b-cell leukemia transcription factor 1 (PBX1) gene.

268/292

<400> 425

```

cttccctgtt tatcctgaaa aggatttgaa g acaagcttg aaggataaaa agccttggtg 60
cttcccagga gccgagccga ggagcagaag aggaagagcc gggggtgcc gtagcctttg 120
gagatggacg agcagcccag gctgatgcat tcccatgctg gggtcgggat ggccggacac 180
cccggcctgt cccagcactt gcaggatggg gccggaggga ccgaggggga gggcgggagg 240
aagcaggaca ttggagacat tttacagcaa attatgacca tcacagacca gagtttggat 300
gaggcgcagg ccagaaaaca tgctttaaac tgccacagaa tgaagcctgc cttgtttaat 360
gtgttggtg aaatcaaaga aaaaacagtt ttgagtatcc gaggagccca ggaggaggaa 420
cccacagacc cccagctgat gcgctggac aacatgctgt tagcggaagg cg tggcgggg 480
cctgagaagg gcgaggggtc gcggcagcg gcggcagcg cggcggcttc tggaggggca 540
ggttcagaca actcagtgga gcattcagat tacagagcca aactctcaca gatcagacaa 600
atctaccata cggagctgga gaaatacagag caggcctgca acgagttcac caccacgtg 660
atgaatctcc tgcgagaca aagccggacc aggccatct ccccaaagga gattgagcgg 720
atggtcagca tcatccaccg caagttcagc tccatccaga tgcagctcaa gcagagcacg 780
tgcgaggcgg tgatgatcct gcgttccga tttctggatg cgcgcgga gagacggaat 840
ttcaacaagc aagcgacaga aatcctgaat gaatatttct attccatct cagcaaccct 900
taccacagtg aggaagccaa agaggagtta gccaaagaat gtggcatcac agtctcccag 960
gtatcaaact ggtttgaaa taagcgaatc cgttacaaga agaacatagg taaatttcaa 1020
gaggaagcca atatttatg tgccaaaaca gctgtcactg ctaccaatgt gtcagcccat 1080
ggaagccaa ctaactcgcc ctcaactccc aactcggctg gttcttcca g ttttttaac 1140
atgtcaaact ctggagattt gttcatgagc gtgcagtcac tcaatgggga ttcttaccaa 1200
ggggcccagg ttggagccaa cgtgcaatca caggtggata cccttcgcca tggtatcagc 1260
cagacaggag gatacagtga tggactcgca gccagtcaga tgtacagtc gcagggcatc 1320
agtgttaatg gaggttggca gga tgctact acccctcat cagtgcctc cctacagaa 1380
ggccctggca gtgttactc tgatacctc aactgatctc ccagcaatcg catcccggct 1440
gaccctcgc cccagtggg gcaggggcag gagggagggt ttctctccca agctgaagcg 1500
gtcagactgg aggtcgaagc aatcagcaaa cacaataaga gtctccttct cttctcttct 15 60
ttgggatgct atttcagcca atctggacac ttctttatac tctcttcct ttttttctg 1620
ggtagaagcc acccttcct gcctccagct gtcagcctg tttctgcat cttccctgcc 1680
cctgtgcctc tgtcctagac ttccgggggt ccccgccctc tctcatatca ctgaaggata 1740
ttttcaacaa ttagaggaat ttaaagagga aaaaaat tac aaagaaaata ataaaagtgt 1800
ttgtacgttt tcaaaaaaa 1819

```

<210> 426

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(506)

<223> 3' terminal sequence. gli -kruppel family

member gli3 (greig cephalopolysyndactyly syndrome)

(GLI3) gene.

<400> 426

```

taaaaagagg gtggtttgag tgtaacaata ctgattcaaa actgaaatgg aagacagttt 60
ctccctagaa tactttaggg tttttcagag tccttttcca taaa aggaat ataattgaaa 120
cacatctcag ttaggtgaga tgagattgct aaaatacata cagaactaaa aaaacagcca 180
aaacaaagtc agtttaactc cttaactcc taatgatttc cggttggttc agtctttttt 240
tcctaaagcc tattgcataa ctgcaaggga attgctttct tccgctaggg aggtcagcaa 300
agaactcatg tccccgatag cc atgttggt ggtgctcatg gacagcgctg ggaatgggag 360
ggacgcccga gggctgggta aagccggaag aaactatgga aaagggtctca atgatacttg 420
ggctcagggc cccgacatca ggctcgagtg gtcccatct ctatgattgc atcgaagtca 480
atctggtacc ctcccaggcc aggctg 506

```

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<210> 427
<211> 239
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(239)
<223> 5' terminal sequence. gli -kruppel family
member gli3 (greig cephalopolysyndactyly syndr ome)
(GLI3) gene.

<400> 427
ggcagaagga tcacttgagg ccaggcattc aagaccagcc tatgcaagat aatgagacct 60
tgtctctatt taaaaaaca aaagcctggt gtggtggtgc atgcctgtag tctcagcctc 120
ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180
agagacaggg ttccaccacg ttgcccaggg cagtcttgaa ctctgaccc caagtgatc 239

<210> 428
<211> 5054
<212> DNA/RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(5054)
<223> gli-kruppel family member gl i3 (greig
cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428
cgatactacg tgggcatttt tggtcgaaga gagctgaagt aatgagaaga catcatggag 60
gcccagtcac acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120
tgctccactc gaacagatgt gagcgagaaa gccgttgccct ccagcaccac ttctaattgag 180
gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240
cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300
gcctcattga tcaagaaaga gatccatggg tccctgccac acgtggcgga gccctctgtg 360
ccgtaccgag ggacggtg tt tgccatggac cccaggaatg gttacatgga gcccactac 420
caccctcctc atcttttccc tgccttccat cctcctgtac caattgatgc cagacatcat 480
gagggccggt accattacga tccatctccg attcctc

cat tgcatatgac ttccgcctta 540
tctagtagcc ctacgtatcc ggacctgccc ttcattagga tctccccaca ccggaacc cc 600
gctgctgctt ccaggtctcc cttcagccct ccacatccct acattaatcc ctacatggac 660
tatatccgct cttgcacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720
agccctacag atgcgcccc tgcaggagtc agcccagcag aatactatca tcagatggcc 780
ctgctaactg gccagcgag cccctatgca gacatt attc cctcagctgc caccgccggc 840
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aggctgtcag ccaggccgag ccgaaaacgt aactgtcca tatcaccact ctccgatcat 960
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aattcccgta gca gctcttc agcaagtggc tcctatggtc acttatctgc aagtgcaatc 1080
agccctgctt tgagcttcac ctactcttcc gcgcccgtct ctctccacat gcatcagcag 1140
atcctaagcc gacaacagag cttaggttca gcctttggac acagccctcc actcatccac 1200
cctgccccaa cttttccaac acagaggcct attccaggga tccctacggt tc tgaacccc 1260

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gtccagggtca gctccggccc ttctgagttcc tcacagaaca agcccacgag tgagtctgca 1320
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 ctccccagcc caggggctcg ggggcagcag gaacagcccg aaggaacaac ccttgtcaag 1440
 gaggaagggg acaaagatga aagcaaa cag gagcctgaag tcactctatga gacaaactgc 1500
 cactgggaag gctgcgcgag ggagttcgac acccaagagc agcttgtgca ccatataaat 1560
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 gagcagaaac ccttcaaagc ccagtatatg ttggtagtgc atatgagaag acacacgggc 1680
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 aatgagaaac catatgtgtg caaaatccca ggctgcacta agcgttacac agaccaagc 1920
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 cagattgact tcgatgccat catagacgat ggggaccact ccagcctgat gtcggggggc 4620
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 gcgtccctcc cattccagc gctgtccatg ag caccacca acatggctat cggggacatg 4740
 agttctttgc tgacctccct agcgggaagaa agcaaatcc ttgcagttat gcaataggct 4800
 ttaggaaaaa aagactgcaa ccaacggaaa tcaataggag ttgaagagat taaactgact 4860
 ttgttttggc tgttttttta gttctgtatg tatttttagca atctcatctc accttaactga 4920

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gatgtgtttc aattatattc cttttatgga aaaggactct gaaaaaccct aaagtattct 4980
aggagaaaac tgtcttccat ttcagtttg aatcagtatt gttacactca aaccaccctc 5040
tttttaaaaa aaaa 5054

<210> 429
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(271)
<223> 3' terminal sequence. interleukin enhancer
binding factor 1 (ILF1) gene.

<400> 429
aggagacttg ttttactcag agtggaaaat ttggccaggg acaaagtc aa cacaaagaaa 60
caaacaacaa aaaatagcca gaaagagaac agttaagtgc agtcggtga gtcccggcag 120
ttccttcccg gcaactggctc gtccctgggt tctcaagggt ccatgcggcc acagcgtccg 180
tccacctgtc cacgcgagcc acatgctgaa atggagggtg ataaaattca tcaggcagct 240
gctgtaacac ggaaatgtgc agatgcc aga g 271

<210> 430
<211> 193
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(193)
<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,
sw|Q08999|RBL2_HUMAN.

<400> 430
TGTCTACATT TNCCACATA AAAATGAAAC AATNNTTCT CCTCGNGAAA AGATTTTATA 60
TTACTTNAGC NAAAGTCCTT CAAAGNGACT GAGCGNANNT AATAGTNTGA TACGCATAGG 120
NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNTNGNGAT GGCNGTGAAT NCACTGCAAA 180
NAGCATTTGC CCN 193

<210> 431
<211> 184
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(184)
<223> 3' terminal sequence. Homo sapiens CD2 antigen (p50).

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<400> 431
AGTCAAAGCT TTTATTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGCAC 60
ATAAGAAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120
AATCACTTGA TTTATCGCAT CTACACATGA CCNGAGAGGG GACAAGAAAT CTCTAAGTTT 180
TCTG 184

<210> 432
<211> 242
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(242)
<223> 5' terminal sequence. Similar to NM_022641 Homo sapiens
chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1)

<400> 432
ATTCGGCACG ATGACTGGCC AGGGTATAAA AAGGGCCAC AAGAGACCGG CTCTAGGATC 60
CCAAGGCCCA ACTCCCGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120
TCCAGGCTCC CGGAACGTCC CTGATCCTGG NTTTTGNCCT NCTCTNACTG CCCTGGNTTN 180
AANAAGCTNG TGCCNTCCAA ANCGTCCGT TATCCAGGGT TTTTGACCAC GCTATGCTNC 240
AA 242

<210> 433
<211> 329
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(329)
<223> 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 433
AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGC CCCAGGNAAA 60
CTTGACGAC GCCTGCCAGG GNATTTCGGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120
CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180
TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC GACCGTGACC 240
AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300
GCAAAGGCGC AGTGCTTCTC TACAGACTT 329

<210> 434
<211> 247
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature

273/292

<222> (1)..(247)

<223> 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

<400> 434

```
AAATATATCT GAANNNTTA AGTACAGTNT AAAACAGGGT TNTGGCAACA GAAAGTAAAA 60
ACTAACATGG NTGCTATAA ATATGCTGAA GCCTAGTTGT TCAAATGATA CAATTCTCTC 120
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTACACTT TACACACT GT ACACAAAGGG 180
GNTACCTTCT GNGNGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240
TTTGAGG                                         247
```

<210> 435

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(63)

<223> 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 435

```
CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCCAAGCCT GACTATGGAG CTGCTGTGGC 60
TTT                                         63
```

<210> 436

<211> 190

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(190)

<223> 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

<400> 436

```
GAAGAGGAGG NCCTTGGCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60
CCAGGGCTCA GCTGTCACTG GGCAGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120
TATATATGNC CACCCACGG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180
GNAGCACAGG                                         190
```

<210> 437

<211> 176

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(176)

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<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTN TTGCACCTGC 60
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P,
granule membrane protein CD62, SELP

<400> 438

NGGAACATAT GGAGTTTTTA CA AACGCTGC ATTTGACCCG AGTCCTTAAG AGACCTGTCC 60
TTTTCTGGT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120
TACACTGGAC TTAACATATAA TGCAATTGCT GCAGGTTTCC ATAAACACCC ATGANTCAAA 180
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240
CTGTTTCCTG AGTTTGGGAT TGTGGTACAA TCTCAAATTC TCAACCTACC ACCCCTTCCT 300
GTCCACCTC TTCTCTTCTT GTAACACAAG CCACAGAAGC CAGGAGCAAA TGTTCCTGCA 360
GTAGTCTCTG TGCTTTGACT CACCTGTTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P,
granule membrane protein CD62, SELP

<400> 439

GAAAATCCTT TNAATTACGN ATTTNAANAT TGGNCTTTGG GNCATTTGAG GGACAGTGAC 60
TGGGGGCAGG AAGGCCACAG GNGACATGTG GCCTTCTAGC TTNATNCTTG GCCTTCTGCA 120
GCCTCTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCTC 180
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCCTNNA ATCAAAAANT AAAGAGGTNT 300
TTCNATTTCT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTTGGNNCAC 360
TGGTATTCA AGTAACAGGT GAGNNAAAGG ANAGAG 39 6

<210> 440

<211> 337

<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(337)

<223> 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 440

```
AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGGCCAAC CCCCATTCT CCACGTGGAT 180
CCTCTTCCCT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTCTTGA GCTGCAGCTG GCGGGTAGGG CCGGGGCCCC CGCGGGACGT 300
CCAGTACGAC CTGTACTTGA ACGTTNCCAA CAGNGT 337
```

<210> 441

<211> 104

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:prim er

<220>

<221> misc_feature

<222> (1)..(104)

<223> 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

<400> 441

```
TTCCCCCTC CCAGACCACC AGNTTGNCGT TTTGGNAGNT NTNACCGANG GGGTNTTNCA 60
TGTNAGGGNT NCGGNAAAN AGTTNTGAA NCACCAGAAA CCTT 104
```

<210> 442

<211> 223

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(223)

<223> 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

<400> 442

```
AAGCAATGGA TGATTTGATG CTGTCCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGGCC CCTGCACCAG 120
CAGCTCCTAC ACCGCGNGCC CCTGCACCAG CCCCCTCCTG GCCCCTGTCA TCTTCTGTCC 180
CTTCCAGAN AACCTACCAG GGCAGCTACG GTTTCGGTCT G GG 223
```

<210> 443

276/292

<211> 223
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(223)
<223> 5' terminal sequence. Tumor protein p53
(Li-Fraumeni syndrome) (TP53) gene.

<400> 443
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggtc actgaagacc 60
caggtccaga tgaagctccc agaatgccag agntgnctcc ccgcgtggcc cctgcaccag 120
cagctcctac accggcngcc cctgcaccag cccctcctg gccctgtca tcttctgtcc 180
cttccagaa aacctaccag ggcagctacg gtttccgtct ggg

<210> 444
<211> 343
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(343)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(343)
<223> v-erb-b2 avian erythroblastic leukemia viral
oncogene homolog 2 (neuro/glioblastoma derived
oncogene homolog) (ERBB2) gene.

<400> 444
caaggggctg caaactnncc cacacatgac ccagccctc tacagcggta cagtgaggac 60
cccacagtac ccctgcctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cggccccagc ccccttcgcc ccgagaggcc 180
ctctgcctgc tgcccgaact gctggtgcc ctctggaaag gcccaagact ctctccccag 240
ggaagaatgg ggtcgtcaaa gagtttttgc cttt gggggt gccgtgggag aacccccgagt 300
attgacaccc caggggaggg agcttgccct tcagccccac ctt 343

<210> 445
<211> 309
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(309)
<223> 3' terminal séquence.

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<220>
<221> misc_feature
<222> (1)..(309)
<223> zinc finger protein 144 (Mel -18) (ZNF144) gene.

<400> 445
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagagggtg aaaaaagggc 60
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tccctggcct 120
caagttaagg ggggcacggg agcgccnttg acagtcattt tgcgccccct gctggtnгаа 180
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc cccacttgct 240
ntcgaagggg ganttgggna ngtagggtnг gtngcttgan gcccatngga actnggaaaa 300
ccatnggat 309

<210> 446
<211> 268
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(268)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(268)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 446
attatcttgt gaatctactt agaaaaacac acacaagcaa tggtcacaac tataaattta 60
aaccttttgc actaaaaaaa cacaaaacaa caaacacaan accacaggca tgaactgtaa 120
acctgtatta actntgaact ggtcttaagg ttaattctta gcngtcattc agtattttcc 180
tccttgгcaa ctgtaatgtt ttngcacggg ntgatctccc gcngggggta ctagtaatga 240
ctggctgccc gtgtagggag atgcttcc 268

<210> 447
<211> 169
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(169)
<223> 5' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(169)
<223> MAP/microtubule affinity-regulating kinase 3
(MARK3) gene.

<400> 447

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gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat cttctaaatc 60
atgaaattaa agtctgagga cgagagcacg nctgggngcg aaantntgcc tttttntac 120
ggatgcacta cantaaagan gtgcanccta tncgccccct gccctactt 169

<210> 448
<211> 393
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(393)
<223> 3' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(393)
<223> EST N68536 MAX-interacting protein 1 (MXI1) gene.

<400> 448
aagtaattaa gggtagttaa attattttaa gtatacaaag tccaaacagc caggggtaag 60
gtctccaaga ggccttccca gggttaaggga gagggccaca agggaacctt ggagtttgaa 120
agacaaaggg aacacatgac atcaaagtgc aggctagaaa ttccacttag aagaaaataa 1 80
cattactgaa aatattcgta agagtaacaa tagcacatgc acagtgggac tgtgaggaag 240
agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgctg 300
aacttactat gttaactatg atagtgtgtc tacnatagat atcncgatgg ttaaaagctg 360
gtaaaaggta atggttctca aaaccnaaa a tag 393

<210> 449
<211> 217
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(217)
<223> 5' terminal sequence.

<220>
<221> misc_feature
<222> (1)..(217)
<223> EST R81126 lymphotoxin beta receptor (LTBR) gene.

<400> 449
ttaccttggt atctcctact gtagtatgag gaagaatggc tgtaaatgta ttttttgaat 60
tctggnctca cctttgtctc agctaaatgt agccgcatcc gggacacagt ttgtgccaca 120
tgtgccgaga attcctacaa cgagc actgg aactacctga ccattctgcca nctgtgccgc 180
ccctgtgacc cagtgatggg cctcgnctga gantgcc 217

<210> 450
<211> 157
<212> ADN

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(157)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(157)

<223> (POU2F2) gene.

<400> 450

```
nattcggcaa cgnggaaagg aaagaaacta accaacaaaa gagaaaacca aaaataatca 60
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120
aggagtnaca agggaggaaa gaccaaaaaa acaacca                               157
```

<210> 451

<211> 282

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(282)

<223> 5' terminal sequence.

<220>

<221> misc_feature

<222> (1)..(282)

<223> caspase 4, apoptosis -related cysteine protease
(CASP4) (ex CASP1)

<400> 451

```
gagaatctga cagccaggga tatggagtca gcgctgaggg catttgctac cagaccagag 60
cacaagtccct ctgacagcac attcttggtta ctcattgtctc atggcatcct ggagggaatc 120
tgcggaactg tgcatgatga gaaaaaacca gatgtgctgc tttatgacac catcttccag 180
atattcaaca accgcaactt gcctcagtct ngaaggacaa acccaaggtc atcattgtnc 240
agggcttgca gagggtgcaa accttggggg aantttgggg tc                               282
```

<210> 452

<211> 424

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(424)

<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(424)
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452
ttgcttttng caaaactcta cttaatccaa tnggtttttc cctgtacagt agattttcca 60
aatgtaataa actttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgcc 120
ctgtgctgtg tgtgacgtga cgggactttt ctgcaaacac caacatgttg ggaaacttgg 180
ctcgaatctc tgtgccttcg tctttcccat ggggagggga ttctggttcc agggccctc 240
tgtgtatttg cttttttgtt ttggctgaaa ttctcctgga ngtcggtagg ttcagccaag 300
gttttataag ggctgatgtc aatttntctg gtttgccaan ttccaagccc catctncta 360
aatgggcaaa aggaagggtg gatggggccc agcnacagct ttgnacc ga gggctnttgg 420
gtca 424

<210> 453
<211> 435
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(435)
<223> 5' terminal sequence

<220>
<221> misc_feature
<222> (1)..(435)
<223> Integrin, beta 2 (antigen CD18 (p95), lymphocyte
function-associated antigen 1; macrophage antigen
1 (mac-1) beta subunit) (ITGB2)

<400> 453
aggagtcccc cggctgcccc tcacct gtg gcaagtacat ctctgcgcc gagtgccctga 60
agttcgaaaa gggccctnt ggaagaactg cagcgcgccg tgtccgggcc tgcagctgtc 120
gaacaacccc gtgaaggcca ggacctgcaa ggagaggac tcagagggt gctgggtggc 180
ctacacgctg gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg 240
agagtgtgtg gcaggcccca acatgcgcgc catcgtcggg ggcaccgtgg gcaggcatcg 300
tgctgatcgg cattctctctg ctggtcatct gggaaggctc tgatccacct gagcgacctc 360
cgggagttac agcgcttttg agnaggagaa gctcaagtc cagtnggaac aatgattatt 420
ccctttttca agagc 435

<210> 454
<211> 544
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(544)

281/292

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(544)

<223> Protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)

<400> 454

```
gtgtgaccag acatgcaacc gncatctatg gtttctacgn atgnagtgnc aagcagnacg 60
nctnacaaca tcaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggacgt aaaagatctt ctgncctgncc acggaggcct gttccccgga 180
cctgncagtt ctatggnagc agattcggcg ggatcatgcg gccacacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgaccctga caaggacgtg cagggctggg 300
gcgagaaacga ccgtgggcgt ctcttttac c tttggagccg aggtggtggc caagttcctc 360
cacaagcacg acttgacact catctgccga gcacaccagg ttgtagaaga cggctacgag 420
ttctttgccg agcggcantt ggtgacactt ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgccatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn 544
```

<210> 455

<211> 344

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(344)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(344)

<223> protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)

<400> 455

```
actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cacgaggaac 60
cgcgcgcggc gngtgcgngt aggcccggtg n gcggtgncgg cgcgggagga gccggannca 120
gccggcnggg gcggngggca ncanggacga gaaggngnnc accaaggagc tggaccagn 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagncc caggncaga gccncagcga 240
gaangcnaaa gaaanccnga caaaagaanc caacngcaa gaggnncgan gnccaggnac 30 0
ngnccngnga gangngcang ggcaannnca ngaacccatg gaac 344
```

<210> 456

<211> 514

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(514)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(514)

<223> S100 calcium-binding protein All (calgizzarin)
(S100A11)

<400> 456

```
cagcctcccc cgctcgctc agctccaaca tggcaaaaat ctccagccct acagagactg 60
agcgggtgcat cgagtccttg attgctgtct tccagaagta tgctggaa ag gatgggttata 120
actacactct ctccaagaca gagttcctaa gcttcatgaa tacagaacta gctgccttca 180
caaagaacca gaaggaccct ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240
gtgatggta gctagatttc tcagaatttc ttaatctgat tggtaggcta gctatggctt 300
gccatggact ccttcctcaa ggctgtccct tcccagaagc gggacctgga gggacccctt 360
gggccttggg cctttcaaac ccacccctn ttcctttcca gcctttctgt tcatcatntt 420
ccacagccca cccttncctg gaggcacatt aaccacctna tggtagggtn ccaactggtc 480
attagttatt aaaggnaatg tnaatttttt ttaa 514
```

<210> 457

<211> 359

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(359)

<223> 5' terminal sequence

<220>

<221> misc_feature

<222> (1)..(359)

<223> Granzyme A (granzyme 1, cytotoxic
T-lymphocyte-associated serine esterase 3) (GZMA)

<400> 457

```
gctggagctc atcaacaagc attcattcaa caacttccgc ctgcgagtgg ggttgaacca 60
tggaaccgta gtagctggag ttattggggc ccagaagccg caatatgaca ttgggggcaa 120
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtgac 180
tgaggagaca gcatggggcc tacagtcctt gggctacacc tgctacagcc nggggtgtca 240
tcanggtgaa aggcaaaggg cagctctgca cctacttcct gaacacagac ttgacacgaa 300
ctggacctcc ttcagctacc ctaggctgag attgcactcg cct tncctaag aacctnaat 359
```

<210> 458

<211> 1251

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(1251)

<223> 3' terminal sequence

<220>

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<221> misc_feature

<222> (1)..(1251)

<223> endothelin 1 (EDN1)

<400> 458

```
ggagctgtttt acccccactc taataggggt tcaatataaa aagccggcag agagctgtcc 60
aagtacagacg cgcctctgca tctgcgccag gcgaacgggt cctgcgcctc ctgcagtccc 120
agctctccac caccgcgcg tgccctgca gacgctccgc tcgctgcctt ctctcctggc 180
agggcgtgcc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg 240
aggaaccgcg agcgctttga gggacctgaa gctgtttttc ttctgtttcc tttgggttca 300
gtttgaacgg gaggtttttg atcccttttt ttccagaatg attatttgct catgattttc 360
tctctgctgt ttgtggcttg ccaaggagct cc agaaacag cagtcttagg cgctgagctc 420
agcgcggttg gtgagaacgg cggggagaaa cccactccca gtccaccctg ggggctccgc 480
cgggtccaagc gctgctctg ctctgccctg atggataaag agtgtgtcta cttctgccac 540
ctggacatca tttgggtcaa cactcccgag cacgttggtc cgtatggact tggagccct 600
aggtccaaga gagccttgga gaatttactt cccacaaagg caacagaccg tgagaataga 660
tgccaatgtg ctagccaaaa agacaagaag tgctggaatt tttgccaagc aggaaaagaa 720
ctcagggctg aagacattat ggagaaagac tgggaataatc ataagaaagg aaaagactgt 780
tccaagcttg ggaaaaagtg tatttatcag cag ttagtga gaggaagaaa aatcagaaga 840
agttcagagg aacacctaa acaaaccagg tcggagacca tgagaaacag cgtcaaatca 900
tcttttcatt atccaagct gaaaggcaag ccctccagag agcggttatgt gaccacaac 960
cgagcacatt ggtgacagac ttctgggctt gctctgaagc atagcctcca cggagagccc 1020
tgtggccgac tctgactct ccacctggc tgggatcaga gcaggagcat cctctgctgg 1080
ttctgactg gcaaaggacc agcgtctctg ttcaaaacat tccaagaaag gttaaggagt 1140
tcccccaacc atcttactg gcttccatca gtggttaact ctttggtctc ttctttcatc 1200
tggggatgac aatggacctc tcagcagaaa caca cagtca cattcgaatt c 1251
```

<210> 459

<211> 2145

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2145)

<223> 3' terminal séquence

<220>

<221> misc_feature

<222> (1)..(2145)

<223> Protein tyrosine phosphatase, non -receptor type 6
(PTPN6)

<400> 459

```
cggcagaact gggaccaccg ggggtggtga ggcggcccg cactgggagc tgcattctgag 60
gcttagtccc tgagctctct gcctgccag actagctgca cctctcatt ccctgcgccc 120
ccttctcttc cggaagcccc caggatggtg aggtggtttc accgagacct cagtgggctg 180
gatgcagaga ccctgctcaa gggccgaggt gtccacggta gcttctctggc tcggccagct 240
cgcaagaacc aggtgactt ctgctctcc gtcagggttg gggatcaggt gacctatatt 300
cggatccaga actcagggga tttctatgac ctgtatggag gggagaagt t tgcgactctg 360
acagagctgg tggagtacta cactcagcag cagggtgttg tgcaggaccg cgacggcacc 420
atcatccacc tcaagtacc gctgaactgc tccgatccca ctagttagag gtggtaccat 480
ggccacatgt ctggcgggca ggcagagacg ctgctgcagg ccaagggcga gccctggacg 540
tttcttgtgc gtgaga gcct cagccagcct ggagacttcg tgctttctgt gctcagtgc 600
cagcccaagg ctggcccagg ctccccgctc aggggtcaccc acatcaaggt catgtgcgag 660
ggtggacgct acacagtggg tggtttggag accttcgaca gcctcacgga cctggtggag 720
```

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```

catttcaaga agacggggat tgaggaggcc tcaggcgccct ttgtctacct gcggcagccg 780
tactatgcc aagcgggtgaa tgccgctgac attgagaacc gagtgttga actgaacaag 840
aagcaggagt ccgaggatac agccaaggct ggcttctggg aggagttga gattttgcag 900
aagcaggagg tgaagaactt gcaccagcgt ctggaagggc aacggccaga gaacaagggc 960
aagaaccgct acaagaa cat tctccccttt gaccacagcc gagtgatcct gcagggacgg 1020
gacagtaaca tccccgggtc cgactacatc aatgccaaact acatcaagaa ccagctgcta 1080
ggccctgatg agaacgctaa gacctacatc gccagccagg gctgtctgga ggccacgggc 1140
aatgacttct ggagatggc gtggcaggag aacagccgtg tcacgtcat gaccacccga 1200
gaggtggaga aaggccggaa caaatgcgtc ccatactggc ccgaggtggg catgcagcgt 1260
gcttatggc cctactctgt gaccaactgc ggggagcatg acacaaccga atacaaactc 1320
cgtaccttac aggtctcccc gctggacaat ggagacctga ttcgggagat ctggcattac 1380
cagtacctga gctggccc ga ccatgggggc cccagtgagc ctgggggtgt cctcagcttc 1440
ctggaccaga tcaaccagcg gcaggaaagt ctgcctcacg caggggcccat catcgtgcac 1500
tgcagcgccg gcatcgccg cacaggcacc atcattgtca tcgacatgct catggagaac 1560
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aagaggaggt gagcggtgt gtctcagggt ggccatgcct cagccctgac cctgtggaag 1980
catttcgcga tggacagact cacaacctga acctaggagt gccccattct tt tgtaattt 2040
aaatggctgc atcccccca cctctccctg acctgtata tagcccagcc agggcccagg 2100
cagggccaac ccttctctc ttgtaaataa agccctggga tcaact 2145

```

<210> 460

<211> 2149

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(2149)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(2149)

<223> Transcription factor AP -4 (activating enhancer binding protein 4) (TFAP4)

<400> 460

```

gacctgcaaa cacacacac a cacacacaca cacacacaca cacacacaca catacacacg 60
caccagggca gccgagagac ctccctcccg cccctcccat gccgcctcc ctccctcgc 120
cgccgcccgc gccgccagca tctgggaccg gccgattctg cacctccgtc cgccgctgcc 180
ctttgattcg gatttccatc ttgcattctc cggtgatcg cgggacctgg ct cgtgcaga 240
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ccactaacc cagagactca gcgggaccag gagcgcgga ttcggcgga gatcgccaac 420
agcaacgagc ggagacgcat gcagagcatc aacgcgggat tccagtcct caagaccctc 480
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gaaggcatag gctccccgga catctgggag gacgagaagg cggaggacct gcggcgagg 720
atgattgagc tgcggcagca gctggacaag gagcgctcgg tgcgcatgat gctggaggag 780
caggtgcgct cgctggaggc ccacatgtac ccgaaaagc tcaaggtgat tgcgcagcag 840

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gtgcagctgc agcagcagca ggaacaggtg aggtctgctgc accaggagaa gctggagcgg 900
gaacagcagc agctgcggac ccagcttctg cccctcccg ccccccacca ccacccacg 960
gtgatcgtgc cagcaccgcc tcctcctccc tcccaccaca tcaatgtcgt caccatgggc 1020
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tgtttttct tttttttct ttttttttt tttttacaat tttgaggtct tcgtgttcaa 2040
ggagaagcta ttatattttg ttaagaaagt gggggagaaa aaaaccaaga ggccaccgtg 2100
cctttgtaaa gaaacaaaat aaa gtttga ctttgtttt taaaaaaaa 2149

```

<210> 461

<211> 6478

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(6478)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(6478)

<223> Cyclin D2 (CCND2)

<400> 461

```

agagcgagca ggggagagcg agaccagttt taaggggag accggtgcga gtaaggcagc 60
cccgaggctc tgctcgccca ccacccaatc ctgcctccc ttctgctcca ccttctctct 120
ctgcctcac ctctcccccg aaaacccctt atttagcaa aggaagg agg tcagggggaa 180
gctctccct ccccttccaa aaaacaaaaa cagaaaaacc cttttccagg ccgggaaag 240
caggagggag aggggcggcc gggtggcca tggagctgct gtgccacgag gtggaccgg 300
tccgcagggc cgtgcgggac cgcaacctgc tccgagacga ccgctcctg cagaacctgc 360
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tccaacctta catgcgcaga atggtggcca cctggatgct ggaggtctgt gaggaacaga 480
agtgcgaaga agaggtcttc cctctggcca tgaattacct ggaccgttct ttggctggg 540
tccgactcc gaagtccat ctgcaactcc tgggtgctgt ctgcatgt tc ctggcctcca 600
aactcaaga accagcccg ctgaccggc agaagctgt catttacacc gacaactcca 660
tcaagcctca ggagctgctg gagtgggaa tgggtggtgct ggggaagtgt aagtggaa 720
tggcagctgt cactcctcat gacttcatt agcacatctt gcgcaagctg cccagcagc 780
gggagaagct gtctc tgaac cgcaagcat ctcagacctt cattgctctg tgtgccaccg 840
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```

<210> 462

<211> 3490

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(3490)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(3490)

<223> Junction plakoglobin (JUP)

<400> 462

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gtcccaccac cggcccagcc ccgaccgcgc cgggtcaggc cccatactca gtagccacga 120
tgagggtgat gaacctgatg gacgagccta tcaaggtagc tgagtggcag cagacataca 180
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agctgctcaa gtcggccatt gtgcatctca tcaactacca ggacgatgcc gagctggcca 540
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aggcgcccat gattgtgaac cagctgtcga agaaggaggg gtcgcgggcg gccctgatgg 660
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```

<210> 463

<211> 1355

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature
<222> (1)..(1355)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1355)
<223> Growth arrest and DNA -damage-inducible, alpha
(GADD45A)

<400> 463
cagtggtgctgg taggcagtggt ctgggaggca gcgggccaat tagtgtcgtg cggcccgtgg 60
cgaggcgagg tccgggggagc gagcgagcaa gcaaggcggg aggggtggcc ggagctgcgg 120
cggttgccac aggaggagga gcccgggcgg gcgaggggag gccggagagc gccagggcct 180
gagctgcccgg agcggcgccct gtgagtgagt gcagaaagca ggcgcccgcg cgctagccgt 240
ggcaggagca gccgcacgc cgcgtctctt ccctgggcga cctgcagttt gcaatatgac 300
tttgaggagaa ttctcggctg gagagcagaa gaccgaaagg atggataagg tgggggatgc 360
cctggaggaa gtgctcagca aagccctgag tc agcgcacg atcactgtcg ggggtgtacga 420
agcggccaag ctgctcaacg tcgacccccga taacgtgggtg ttgtgcctgc tggcggcgga 480
cgaggacgac gacagagatg ttgctctgca gatccacttc accctgatcc aggcgttttg 540
ctgcgagaac gacatcaaca tctgcgcgt cagcaaccgg ggccggctgg cggagctcct 600
gctcttggag accgacgtg gccccgcggc gagcgagggc gccgagcagc ccccggaact 660
gcactgcgtg ctggtgacga atccacattc atctcaatgg aaggatcctg ccttaagtca 720
acttattttg ttttgccggg aaagtcgcta catggatcaa tgggttccag tgattaatct 780
cctgaacgg tgatggcatc tgaatgaaaa taa ctgaacc aaattgcact gaagtttttg 840
aaataccttt gtagttactc aagcagttac tccctacact gatgcaagga ttacagaaac 900
tgatgccaag gggctgagtg agttcaacta catgttcttg gggcccgag atagatgact 960
ttgcagatgg aaagagggtga aaatgaagaa ggaagctgtg ttgaaacaga aaaataagtc 1020
aaaaggaaca aaaattacaa agaaccatgc aggaaggaaa actatgtatt aatttagaat 1080
ggttgagtta cattaaaata aaccaaatat gttaaagttt aagtgtgcag ccatagtttg 1140
ggtatttttg gtttatatgc cctcaagtaa aagaaaagcc gaaagggtta atcatatttg 1200
aaaaccatat tttattgtat tttgatgaga tatt aaattc tcaaagtttt attataaatt 1260
ctactaagtt attttatgac atgaaaagtt atttatgcta taaatttttt gaaacacaat 1320
acctacaata aactggatat aataattgca tcatt 1355

<210> 464
<211> 732
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(732)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(732)
<223> Non-metastatic cells 1, protein (NM23A) expressed
in (NME1)

<400> 464
tgctgcgaac cacgtgggtc cggggcgcgt ttccgggtgct ggccggtgca gccggagttc 60
aaacctaagc agctggaagg aaccatggcc aactgtgagc gtaccttcat tgcatcaaaa 120
ccagatgggg tccagcgggg tcttggtgga gagattatca agcgttttga gcagaaagga 180
ttccgccttg ttggtctgaa attcatgcaa gcttccgaag atcttctcaa ggaacactac 240
gttgacctga aggaccgtcc attctttgcc ggccgtggtga aatacatgca ctcagggccg 300

290/292

gtagttgcc a tggctctggga ggggctgaat gtgggtgaaga cgggccgagt catgctcggg 360
 gagaccaacc ctgcagactc caagcctggg accatccgtg gagacttctg catacaagtt 420
 ggcaggaaca ttatacat gg cagtgattct gtggagagtg cagagaagga gatcggcttg 480
 tggtttcacc ctgaggaact ggtagattac acgagctgtg ctcagaactg gatctatgaa 540
 tgacaggagg gcagaccaca ttgcttttca catccatttc cctccttcc catgggcaga 600
 ggaccaggct gtaggaaatc tagttattta caggaacttc atcataattt g gaggggaagc 660
 tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgaccatct gattaaaatg 720
 ctctctccca gc

<210> 465

<211> 942

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(942)

<223> 3' terminal sequence

<220>

<221> misc_feature

<222> (1)..(942)

<223> Ribosomal protein L13 (RPL13) (ex BBC1)

<400> 465

ctttccgctc ggctgttttc ctgcgcagga gccgcagggc cgtaggcagc catggcgccc 60
 agccggaatg gcatggtctt gaagccccac ttccacaagg actggcagcg gcgcgtggcc 120
 acgtggttca accagccggc ccgtaagatc cgcagacgta aggcccggca agccaaggcg 180
 cgccgcatcg ccccgcgccc cgctcggtt cccatccggc ccacgtgcy ctgcccacg 240
 gttcggatcc acacgaaggc gcgcgcggc cgcggttca gcctggagga gtcagggtg 300
 gccggcattc acaagaaggc ggcccgacc atcggcattt ctgtggatcc gaggaggcgg 360
 aacaagtcca cggagtccct gcagaccaac gtgcagcggc tgaaggagta ccgctccaaa 420
 ctcatcctct tccccaggaa gccctcggcc cccaagaagg gagacagttc tgctgaagaa 480
 ctgaaactgg ccacccagct gaccggaccg gtcatgcccg tccggaacgt ctataagaag 540
 gagaaagctc gagtcacac tgaggaagag aagaatttca aagccttcgc tagtctccgt 600
 atggcccgty ccaacgccc gctcttcggc atacgggcaa aaagagccaa ggaagccgca 660
 gaacaggatg ttgaaaagaa aaaataaagc cctcctgggg acttggaaac agtcgggcag 720
 tcatgtggg tctccacgtg gtgtgtttcg tgggaacaac tgggcctggg atggggcttc 780
 actgctgtga cttcctctc ccaggggatt tggggctttc ttgaaagaca gtccaagccc 840
 tggataatgc tttactttct gtgttgaagc actgttggtt gtttggttag tgactgatgt 900
 aaaacggttt tcttggtggg aggttacaga ggctgacttc ag 942

<210> 466

<211> 755

<212> ADN

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc_feature

<222> (1)..(755)

<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(755)
<223> vascular endothelial growth factor B (VEGFB)m

<400> 466
caccatgagc cctctgctcc gccgcctgct gctcgccgca ctcttgacgc tggccccgc 60
ccaggccccct gtctcccagc ctgatgcccc tggccaccag aggaaagtgg tgatcatggat 120
agatgtgtat actcgcgcta cctgccagcc ccgggaggtg gtggtgccct tgactgtgga 180
gctcatgggc accgtggcca aacagctggt gccagctgc gtgactgtgc agcgtgtgg 240
tggctgctgc cctgacgatg gcctggagtg tgtgcccact gggcagcacc aagtccggat 300
gcagatcctc atgatccggt acccgagcag t cagctgggg gagatgtccc tggaagaaca 360
cagccagtgt gaatgcagac ctaaaaaaaaa ggacagtgtc gtgaagccag acagggctgc 420
cactccccac caccgtcccc agccccgttc tgttccgggc tgggactctg cccccggagc 480
accctcccca gctgacatca cccatcccac tccagcccca ggccccctctg cccacgtgc 540
accagcacc accagcgccc tgacccccgg acctgccgc gccgtgccg acgcccgcagc 600
ttcctccgtt gccaaagggc gggttagag ctcaaccag acacctgcag gtgccggaag 660
ctgcgaaggt gacacatggc ttttcagact cagcaggtg acttgccca gaggtatat 720
cccagtgggg gaacaaagag gagcctggta aa aaa 755

<210> 467
<211> 1039
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(1039)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(1039)
<223> Laminin receptor 1 (67kD, ribosomal protein SA)
(LAMR1)

<400> 467
tgccctgtctt ttccgtgcta cctgcagagg ggtccatacg gcgttgttct ggattcccgt 60
cgtaacttaa agggaaactt tcacaatgtc cggagccctt gatgtcctgc aaatgaagga 120
ggaggatgtc cttaa gttcc ttgcagcagg aaccactta ggtggcacca atcttgactt 180
ccagatggaa cagtacatct ataaaaggaa aagtgatggc atctatatca taaatctcaa 240
gaggacctgg gagaagcttc tgctggcagc tcgtgcaatt gttgccattg aaaaccctgc 300
tgatgtcagt gttatatcct ccaggaatac tggccagagg gctgtgctg a agtttgctgc 360
tgccactgga gccactcaa ttgctggccg cttcactcct ggaaccttca ctaaccagat 420
ccaggcagcc ttccgggagc caccgcttct tgtggttact gaccccaggg ctgaccacca 480
gcctctcacg gaggcattct atgttaacct acctaccatt gcgtgtgta acacagattc 540
tcctctgcgc tatgtg gaca ttgccatccc atgcaacaac aaggagctc actcagtggg 600
tttaatgtgg tggatgctgg ctcggaagt tctgcgcatg cgtggcacca tttcccgatga 660
acacccatgg gaggtcatgc ctgatctgta cttctacaga gatcctgaag agattgaaaa 720
agaagagcag gctgctgctg agaaggcagt gaccaaggag gaatttcagg gtgaatggac 780
tgctcccgtc cctgagttca ctgctactca gcctgagggt gcagactggg ctgaagggtg 840
acaggtgccc tctgtgccta ttcagcaatt ccctactgaa gactggagcg ctgagcctgc 900
cacggaagac tggctgcag ctcccactgc tcaggccact gaatgggtag gagcaaccac 960
tgactggtct taagctg ttc ttgcataggc tcttaagcag catggaaaaa tggttgatgg 1020
aaaataaaca tcagtttct 1039

<210> 468
<211> 240
<212> ADN
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> misc_feature
<222> (1)..(240)
<223> 3' terminal sequence

<220>
<221> misc_feature
<222> (1)..(240)
<223> Chorionic somatomammotropin hormone 1 (placental
lactogen) = LACTOGEN Precursor

<400> 468
attcggcacg atgactggcc aggggtataaa aagggccac aagagac cgg ctctaggatc 60
ccaaggccca actccccgaa ccactcaggg tctgtggca gtcacctag tggcaatggc 120
tccaggtcc cggaacgtcc ctgactctgg nttttgncct nctctnactg ccctggnttn 180
aanaagctng tgccttccaa ancgttcgt tatccagggt ttttgaccac gctatgctnc 240

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